

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 106.251 Seconds
(without alignments)

487.964 Million cell updates/sec

Title: US-10-700-632-7

Perfect score: 622

Sequence: 1 QVQLQQPGAEVWVPGASVKM.....EVRLRYFDVWVGAGTIVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	622	100.0	118	ADO32091	Ado32091 Mouse ant
2	618	99.4	117	ADO32157	Ado32157 Mouse ant
3	613	98.6	118	ADO32093	Ado32093 Humanised
4	536.5	86.3	121	ADJ94605	Adj94605 Chimeric
5	536.5	86.3	121	ADJ94607	Adj94607 Chimeric
6	534.5	85.9	140	AAR55215	Aar55215 Murine va
7	534.5	85.9	412	AAB30694	Aab30694 A fusion
8	534.5	85.9	412	ABJ39009	Abj39009 B9E9 scFv
9	533.5	85.8	140	ABR55873	AbR55873 Anti-CD20
10	533.5	85.8	140	ABU08394	Abu08394 Murine an
11	533.5	85.8	140	ADC66270	Ade66270 Mouse ant
12	533.5	85.8	140	ADCE85690	Ade85690 Murine im
13	533.5	85.8	140	ADE73084	Ade73084 Murine FU
14	533.5	85.8	140	ADF60661	Adf60661 Protein r
15	533.5	85.8	140	ADN49734	Adn49734 Mature va
16	533.5	85.8	140	ADU74410	Adu74410 Mouse ant
17	533.5	85.8	140	ADV92492	Adv92492 2B8 heavy
18	533.5	85.8	140	ADV98555	Adv98555 Novel chi
19	533.5	85.8	140	ADZ59909	Adz59909 Glycoprot
20	533.5	85.8	360	AAE27924	Aae27924 Human CH2
21	533.5	85.8	360	ABB82833	Abb82833 Antibody
22	533.5	85.8	368	ADW77074	Adw77074 Heavy cha
23	533.5	85.8	451	ADL92472	Adl92472 Antibody
24	533.5	85.8	451	ADL92473	Adl92473 Improved

25	533.5	85.8	451	8	ADU68155	Adu68155 Novel var
26	533.5	85.8	451	8	ADU68154	Adu68154 Novel var
27	533.5	85.8	470	3	AAB08026	Aab08026 A dimeric
28	533.5	85.8	470	5	AAE27923	Aae27923 Human C2B
29	533.5	85.8	470	6	ABB82832	Abb82832 Antibody
30	533.5	85.8	470	9	ADV92496	Adv92496 Anti-CD20
31	533.5	85.8	470	9	ADV98559	Adv98559 Novel chi
32	533.5	85.8	626	9	ADV92500	Adv92500 CD20VH/FC
33	533.5	85.8	626	9	ADV98563	Adv98563 Novel chi
34	533.5	85.8	641	9	ADV92502	Adv92502 CD20VH/FC
35	533.5	85.8	641	9	ADV98565	Adv98565 Novel chi
36	533.5	85.8	657	9	ADV92504	Adv92504 FL/FC/CD2
37	533.5	85.8	657	9	ADV98567	Adv98567 Novel chi
38	531.5	85.5	120	7	ADJ94601	Adj94601 Mouse ant
39	530.5	85.3	423	4	AAB30695	Aab30695 A fusion
40	530.5	85.3	423	6	ABJ39010	Abj39010 B9E9 scFv
41	527	84.7	123	6	AAO27201	Aao27201 Murine an
42	526.5	84.6	121	9	ADX16286	Adx16286 2B8 antib
43	521	83.8	122	9	ADV21492	Adv21492 Human ant
44	521	83.8	122	9	ADX16294	Adx16294 Lue16 ant
45	521	83.8	122	9	ADZ83548	Adz83548 CD20 VH.

ALIGNMENTS

RESULT 1

ADO32091

ID ADO32091 standard; protein; 118 AA.

XX AC ADO32091;

XX AC ADO32091;

DT 12-AUG-2004 (first entry)

DE Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

XX anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;

KW heavy chain.

XX Mus musculus.

XX WO2004043344-A2.

XX WO2004043344-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

XX N-PSDB; ADO32140.

XX New antibodies that bind to CD33, useful for treating a disease

PT associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.

XX Claim 5; SEQ ID NO 7; 124pp; English.

PS The present invention describes an isolated anti-CD33 antibody or its

CC epitope-binding fragment comprising: (a) at least one complementarity-

CC determining region (CDR); or (b) at least heavy chain variable region

CC comprising 3 CDRs, and at least one light chain variable region, where

CC the CDR has the ability to bind CD33. Also described: (1) an

CC immunocnjugate comprising the antibody or its epitope-binding fragment

CC linked to a drug or prodrug; (2) a composition comprising the antibody or

CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

composition comprising the immunoconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment defined above; (9) an isolated polynucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polynucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) obtaining CD33 from a biological material. The anti-CD33 antibody has cytostatic activity. The antibody or its epitope-binding fragment, immunoconjugate, composition can be used for treating a subject having a disease where CD33 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. It can also be used for inhibiting the growth of cells expressing CD33, and for *in vivo* imaging or as affinity purification agents. The present sequence represents the mouse anti-CD33 antibody My9-6 heavy chain variable region, which is used in an example from the present invention.

	Query Match	100.0%	Score 622;	DB 8;	Length 118;
	Best Local Similarity	100.0%;	Pred. No. 2.6e-45;		
	Matches 118;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHIMIKPTPGGLEWGVIVPGNDDISY	60		
Db	1	QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHIMIKPTPGGLEWGVIVPGNDDISY	60		
QY	61	NQKFGKATLTADKSSITAYNQLSSLTSEDSAVYICAREVRLRYFDWGAGTTVTVSS	118		
Db	61	NQKFGKATLTADKSSITAYNQLSSLTSEDSAVYICAREVRLRYFDWGAGTTVTVSS	118		

RESULT 2	
ADO32157	
ID	ADO32157 standard; protein; 117 AA.
XX	
AC	ADO32157;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.
XX	
KW	anti-CD33 antibody; epitope-binding fragment;
KW	complementarity-determining region; CDR; immunoconjugate; cytostatic;
KW	antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW	chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.
XX	
OS	Mus musculus.
XX	
PN	WO2004043344-A2.
XX	
PD	27-MAY-2004.
XX	
PF	05-NOV-2003; 2003WO-US032737.
XX	
PR	07-NOV-2002; 2002US-0424332P.
XX	
PA	(IMMU-) IMMUNOGEN INC.
XX	
PI	Hoffee MG, Tavares D, Lutz RJ;
XX	
DR	WPI; 2004-411619/38.
XX	
PT	New antibodies that bind to CD33, useful for treating a disease
PT	associated with CD33 expression, such as myelodysplastic syndrome, acute

PN WO2004043344-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 XX Hoffee MG, Tavares D, Lutz RJ;
 PI WPI; 2004-411619/38.
 XX
 DR
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX
 PS Claim 11; SEQ ID NO 9; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy
 CC chain variable region, which is used in an example from the present
 CC invention.
 XX
 SQ Sequence 118 AA;
 Query Match 98.6%; Score 613; DB 8; Length 118;
 Best Local Similarity 98.3%; Pred. No. 1.5e-44;
 Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKQTPGGGLEWVGVIYFGNDISY 60
 DB 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKQTPGGGLEWVGVIYFGNDISY 60
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR--YFDVWGAGTTVTSS 118
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR--YFDVWGAGTTVTSS 118
 RESULT 4
 ADJ94605
 ID ADJ94605 standard; protein; 121 AA.
 XX

AC ADJ94605;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Chimeric anti-CD20 antibody variable heavy chain.
 XX
 KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
 KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
 KW thrombocytopenia; lupus; rheumatoid arthritis;
 KW heavy chain variable region.
 XX
 OS Chimeric.
 OS Unidentified.
 XX
 PN WO2003068821-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 14-FEB-2003; 2003WO-GH000665.
 XX
 PR 14-FEB-2002; 2002US-0356132P.
 PR 07-OCT-2002; 2002US-0416232P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 PA (MCCA/) MCCALL J D.
 XX
 PI Hansen H, Qu Z, Goldenberg DM;
 DR WPI; 2003-697522/66.
 DR N-PSDB; ADJ94604.
 XX
 PT New humanized anti-CD20 monoclonal antibody (MAb) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune diseases.
 XX
 PS Disclosure; Fig 2B; 106pp; English.
 XX
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (MAb) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 MAb variable
 CC region and the framework regions (FRs) of at least one human IV1AB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a chimeric anti-CD20 antibody
 CC variable heavy chain.
 XX
 SQ Sequence 121 AA;
 Query Match 86.3%; Score 536.5; DB 7; Length 121;
 Best Local Similarity 84.3%; Pred. No. 5e-38;
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKQTPGGGLEWVGVIYFGNDISY 60
 DB 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKQTPGGGLEWIGAIYFGNGDTSY 60
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR--YFDVWGAGTTVTSS 117
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR--YFDVWGAGTTVTSS 120
 QY 118 \$ 118
 DB 121 \$ 121
 RESULT 5
 ADJ94607
 ID ADJ94607 standard; protein; 121 AA.
 XX
 ADJ94607;
 XX

DT 06-MAY-2004 (first entry)
 XX Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.
 DE
 KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
 XX IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
 KW thrombocytopenia; lupus; rheumatoid arthritis;
 KW heavy chain variable region.
 XX
 OS Chimeric.
 OS Unidentified.
 XX
 PN WO2003068821-A2.
 XX
 PD 21-AUG-2003.
 XX
 XX 14-FEB-2003; 2003WO-GB000665.
 XX
 PR 14-FEB-2002; 2002US-0356132P.
 PR 07-OCT-2002; 2002US-0416232P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 PA (MCCA/) MCCALL J D.
 XX
 XX Hansen H, Qu Z, Goldenberg DM;
 PI WPI; 2003-697522/66.
 DR
 XX New humanized anti-CD20 monoclonal antibody (MAb) that retains
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
 PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
 PT leukemia or an autoimmune disease.
 XX
 XX Claim 22; Fig 4A; 106pp; English.
 PS
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
 CC (MAb) or its antigen-binding fragment containing the complementarity
 CC determining regions (CDRs) of at least one murine anti-CD20 MAb variable
 CC region and the framework regions (FRs) of at least one human IV1AB
 CC variable region. The antibodies of the invention are useful for
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
 CC present amino acid sequence represents a chimeric anti-CD20 antibody
 CC variable heavy chain.
 XX
 SQ Sequence 121 AA;
 Query Match 86.3%; Score 536.5; DB 7; Length 121;
 Best Local Similarity 84.3%; Pred. No. 5e-38;
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGQLEWGVVYIPGNDISY 60
 DB 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGQLEWGVVYIPGNDISY 60
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---YFDVWGAGTTVTVS 117
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---YFDVWGAGTTVTVS 117
 QY 118 S 118
 DB 121 S 121
 RESULT 6
 AAR55215
 ID AAR55215 standard; protein; 140 AA.
 AC
 AC AAR55215;
 XX
 XX 25-MAR-2003 (revised)
 DT 01-FEB-1995 (first entry)
 DT
 XX

DE Murine variable region heavy chain from 2BS.
 XX
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 cell lysis.
 XX
 OS Mus musculus.
 XX WO9411026-A2.
 PN
 XX 26-MAY-1994.
 PD
 XX 12-NOV-1993; 93WO-US010953.
 PF
 XX 13-NOV-1992; 92US-00978891.
 PR 03-NOV-1993; 93US-00149099.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Anderson DR, Rastetter WH, Hanna N, Leonard JE, Newman RA;
 PI Ref ME;
 PI
 XX WPI; 1994-183162/22.
 DR N-PSDB; AAQ65631.
 DR
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing
 PT rapid depletion of peripheral B cells, also new antibodies and
 PT hybridomas.
 PT
 XX Disclosure; Fig 5; 101pp; English.
 PS
 XX The sequence is the murine variable region heavy chain derived from
 CC murine anti-CD20 monoclonal antibody 2BS. See also AAQ65629-35. (Updated
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX
 SQ Sequence 140 AA;
 Query Match 85.9%; Score 534.5; DB 2; Length 140;
 Best Local Similarity 83.5%; Pred. No. 8.6e-38;
 Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
 QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGQLEWGVVYIPGNDISY 60
 DB 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGQLEWGVVYIPGNDISY 79
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---RYFDVWGAGTTVTVS 117
 DB 80 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---RYFDVWGAGTTVTVS 139
 QY 118 S 118
 DB 140 A 140
 RESULT 7
 AAB30694
 ID AAB30694 standard; protein; 412 AA.
 XX
 AC AAB30694;
 XX
 XX 02-APR-2001 (first entry)
 DT
 XX A fusion of anti-CD20 single chain antibody/streptavidin.
 DE
 XX Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; B9E9.
 KW
 XX Synthetic.
 OS Streptomyces avidinii.
 OS Homo sapiens.
 XX
 XX Key
 FT Protein
 FT 1. .108

FT Peptide /note= "VL chain"
 FT 109. .126
 FT Protein /note= "linker"
 FT 127. .248
 FT Peptide /note= "VH chain"
 FT 249. .253
 FT Protein /note= "linker"
 FT 254. .412
 FT /note= "streptavidin"
 XX WO200075333-A1.
 PN 14-DEC-2000.
 XX 05-JUN-2000; 2000WO-US015595.
 XX 07-JUN-1999; 99US-0137900P.
 PR 03-DEC-1999; 99US-0168976P.
 XX (NEOR-) NEORX CORP.
 PA Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 PI WPI; 2001-091213/10.
 XX N-PSDB; AAC86563.
 DR New vector constructs for expressing genomic streptavidin fusion proteins
 PT which are useful for targeting tumor cells associated with cancer, e.g.
 PT adenocarcinomas.
 XX Example 2; Fig 11B; 100pp; English.
 PS The present sequence represents a fusion of an anti-CD20 single chain
 XX antibody (B9E9) streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 CC nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 CC nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic acid
 CC sequence. Alternatively, the vector construct comprises a nucleic acid,
 CC operatively linked to a promoter, encoding a polypeptide to be fused with
 CC streptavidin, and a cloning site for insertion of a second nucleic acid
 CC encoding at least 129 amino acids of streptavidin or its functional
 CC variant. The fusion proteins are useful for targeting tumour cells,
 CC particularly tumour cells associated with cancer, e.g. adenocarcinomas or
 CC hematological malignancies. The vector construct is useful for expressing
 CC of streptavidin fusion proteins. In particular, these are useful as tools
 CC for medical diagnostics and therapeutic purposes, e.g. for detecting the
 CC presence or absence of, or treating, a target site within a mammalian
 CC host
 XX Sequence 412 AA;
 SQ Query Match 85.9%; Score 534.5; DB 4; Length 412;
 Best Local Similarity 85.2%; Pred. No. 2.6e-37;
 Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;
 QY 1 QVQLQPGAEVRFPGASVKMSCKASGYTFSTSYIHNIKQTPGQGLEWVGVIYFGNDISY 60
 Db 128 QVQLVQSGAEVRFPGASVKMSCKASGYTFSTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 187
 QY 61 NQPKFGKATLTADKSSTTAYMQLSSLTSEDSAVVYICAREVRLR----YFDVWGAGTIVTV 116
 Db 188 NQPKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYICAR-AQLRPNTWYFDVWGAGTIVTV 246
 QY 117 SS 118
 Db 247 SS 248
 RESULT 8
 ABJ39009

ID ABJ39009 standard; protein; 412 AA.
 XX AC ABJ39009;
 XX DT 09-OCT-2003 (first entry)
 XX DE B9E9 scFvSA fusion protein A amino acid sequence.
 KW Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scFvSA;
 KW anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy;
 KW cell-specific targeting agents; single chain; tumour; B9E9.
 XX Streptomyces avidinii.
 OS Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Region 1. .106
 FT /note= "VL region of the fusion protein"
 FT Region 107. .127
 FT /note= "Synthetic linker region (PKOD)"
 FT Region 128. .247
 FT /note= "VH region of the fusion protein"
 FT Region 248. .253
 FT /note= "Synthetic linker region"
 FT Region 254. .412
 FT /note= "Streptavidin region of the fusion protein"
 XX WO2003050260-A2.
 XX 19-JUN-2003.
 XX 06-DEC-2002; 2002WO-US039429.
 XX 07-DEC-2001; 2001US-00013173.
 PR 17-MAY-2002; 2002US-00150762.
 PR 16-SEP-2002; 2002US-00244821.
 XX (NEOR-) NEORX CORP.
 XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 PI Dearstyne EA;
 XX WPI; 2003-532908/50.
 XX N-PSDB; ABT43498.
 XX New vector construct for expressing genomic streptavidin fusion proteins
 PT useful as diagnostic markers or as cell-specific targeting agents.
 XX Disclosure; Fig 11B; 156pp; English.
 XX This invention relates to novel vector constructs for the expression of
 CC streptavidin fusion proteins. Streptavidin (SA) is produced by
 CC Streptomyces avidinii and specifically binds water-soluble biotin. The
 CC vectors comprise a nucleic acid sequence encoding genomic streptavidin, a
 CC promoter operatively linked to the nucleic acid sequence and a cloning
 CC site for insertion of a second nucleic acid sequence encoding an anti-
 CC CD25 antibody or its antigen binding fragment. The fusion proteins
 CC encoded are known as single chain antibody-genomic streptavidin fusion
 CC proteins (scFvSA). The vectors may have cytostatic activity when used in
 CC gene therapy. The vectors may be useful in expressing genomic
 CC streptavidin fusion cassettes. The fusion proteins may be used as
 CC diagnostic markers or as cell-specific targeting agents. These may also
 CC be used in treating tumours. The present sequence is the amino acid
 CC sequence of the B9E9 single chain antibody-genomic streptavidin fusion
 CC protein of the invention
 XX Sequence 412 AA;
 SQ Query Match 85.9%; Score 534.5; DB 6; Length 412;
 Best Local Similarity 85.2%; Pred. No. 2.6e-37;
 Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or
 CC administering, at a second administration period, a radiolabelled anti-
 CC CD20 antibody, to the human subject. The invention also discloses
 CC expression vectors that may be used in the method of the present
 CC invention. The method is useful for treating B cell lymphoma in humans.
 CC The present sequence represents murine anti-CD20 antibody heavy chain
 CC variable region
 XX
 SQ Sequence 140 AA;
 Query Match 85.8%; Score 533.5; DB 6; Length 140;
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;
 Matches 101; Conservative 8; Mismatches 9;
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHMIKQTPGGQLEWVGVIYFGNDISY 60
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHMIKQTPGGQLEWVGVIYFGNDISY 79
 QY 61 NQPFKGRKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117
 DB 80 NQPFKGRKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 139
 QY 118 S 118
 DB 140 A 140
 RESULT 11
 ADC66270
 ID ADC66270 standard; protein; 140 AA.
 XX
 AC ADC66270;
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse anti-CD20 antibody heavy chain variable region.
 XX
 KW immunosuppressant; cytostatic; antibody; CD20;
 KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;
 KW sugar chain; cancer; immune disorder.
 XX
 OS Mus musculus.
 XX
 PN WC2003055993-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 25-DEC-2002; 2002WO-JP013534.
 XX
 PR 25-DEC-2001; 2001JP-00392753.
 PR 09-APR-2002; 2002JP-00106948.
 PR 01-NOV-2002; 2002JP-00319375.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;
 XX
 DR WPI; 2003-559274/52.
 DR N-PSDB; ADC66269.
 XX
 PT Antibody binding to CD20 and having Fc-bound sugar chains of low fucose
 PT content for treatment of cancer and immune disorders.
 XX
 PS Disclosure; SEQ ID NO 14; 200pp; Japanese.
 XX
 CC The invention relates to cells producing an antibody molecule
 CC specifically binding to CD20 are new, in which the antibody contains N-
 CC glycoside bond complex sugar chains bonded to the Fc region of the
 CC antibody peptide chains, of which less than 20% have a fucose residue
 CC bonded to the N-acetylglucosamine residue at the reducing end of the
 CC sugar chain. The cells are used in the treatment and prevention of cancer
 CC and immune disorders. This sequence corresponds to a protein used in the
 CC method of the invention.

XX
 SQ Sequence 140 AA;
 Query Match 85.8%; Score 533.5; DB 7; Length 140;
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;
 Matches 101; Conservative 8; Mismatches 9;
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHMIKQTPGGQLEWVGVIYFGNDISY 60
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHMIKQTPGGQLEWVGVIYFGNDISY 79
 QY 61 NQPFKGRKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117
 DB 80 NQPFKGRKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 139
 QY 118 S 118
 DB 140 A 140
 RESULT 12
 ADE85690
 ID ADE85690 standard; protein; 140 AA.
 XX
 AC ADE85690;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Murine immunoglobulin heavy chain variable region.
 XX
 KW B cell lymphoma; anti-CD20; peripheral B cell; C2B8;
 KW immunoglobulin heavy chain variable region; mouse; antibody.
 XX
 OS Mus sp.
 XX
 PN US2003147895-A1.
 XX
 PD 07-AUG-2003.
 XX
 PF 11-SEP-2002; 2002US-00238681.
 XX
 PR 13-NOV-1992; 92US-00978891.
 PR 03-NOV-1993; 93US-00149099.
 PR 29-AUG-1997; 97US-00921060.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;
 PI Rastetter WH;
 XX
 DR WPI; 2003-897520/82.
 DR N-PSDB; ADE85689.
 XX
 PT Treating B cell lymphoma by administering an anti-CD20 antibody and at
 PT least one chemotherapeutic agent.
 XX
 PS Example; SEQ ID NO 11; 52pp; English.
 XX
 CC The invention relates to an improved method for treating B cell lymphoma
 CC comprising administering an anti-CD20 antibody. The improvement comprises
 CC administering at least one chemotherapeutic agent. The antibody causes a
 CC substantial depletion of peripheral B cells. The antibody is chimeric
 CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.
 CC This sequence represents a murine immunoglobulin heavy chain variable
 CC region used in the method of the invention.
 XX
 SQ Sequence 140 AA;
 Query Match 85.8%; Score 533.5; DB 7; Length 140;
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;
 Matches 101; Conservative 8; Mismatches 9;
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHMIKQTPGGQLEWVGVIYFGNDISY 60

Db 20 QVLOQPGAEIVKPGASVMSCKASGYTFTSYIHWIKOTPGGLEWIGAIYPNGDTSY 79
 QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
 Db 80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139
 QY 118 S 118
 Db 140 A 140

RESULT 13
 ADE73084
 ID ADE73084 standard; protein; 140 AA.
 AC ADE73084;
 DT 29-JAN-2004 (first entry)
 XX Murine FUT8-related sequence.
 DE Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial;
 KW Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour;
 KW allergy; inflammation; autoimmune disease; circulatory disorder;
 KW viral infection; bacterial infection; murine.

OS Mus musculus.
 XX WO2003085107-A1.
 PN 16-OCT-2003.
 PD 09-APR-2003; 2003WO-JP004507.
 PF 09-APR-2002; 2002JP-00106953.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 PA Yamane N, Satoh M, Mori K, Yamano K;
 PI WPI: 2003-833570/77.
 DR N-PSDB; ADE73069.
 XX Cells with reduced or absent alpha 1,6-fucosyltransferase activity for
 PT treatment of tumors, allergy, inflammation, autoimmune disease,
 PT circulatory disorders, and viral and bacterial infection.
 XX Example 6; Page 165-166; 187pp; Japanese.

XX The present invention relates to cells with modified sugar chain
 CC modifying enzyme activity. The enzyme activity of binding the 1-position
 CC of fucose to the 6-position of an N-acetylglucosamine at the reducing end
 CC of a complex N-glycoside linked sugar chain via an alpha-bond is absent
 CC or less than in the parent cell. The sugar chain modifying enzyme is
 CC preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-
 CC ADE73056). The invention is useful for the treatment and prevention of
 CC tumours, allergy, inflammation, autoimmune disease, circulatory
 CC disorders, and viral and bacterial infection. The present sequence was
 CC used in an example from the invention.

SQ Sequence 140 AA;
 Query Match 85.8%; Score 533.5; DB 7; Length 140;
 Best Local Similarity 83.5%; Pred. No. 1e-37;
 Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOQPGAEIVKPGASVMSCKASGYTFTSYIHWIKOTPGGLEWIGAIYPNGDTSY 60
 Db 20 QVLOQPGAEIVKPGASVMSCKASGYTFTSYIHWIKOTPGGLEWIGAIYPNGDTSY 79
 QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117

Db 80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139
 QY 118 S 118
 Db 140 A 140

RESULT 14
 ADF60661
 ID ADF60661 standard; protein; 140 AA.

AC ADF60661;
 DT 12-FEB-2004 (first entry)
 XX Protein related to the invention #2.

DE Cytostatic; antiallergic; immunomodulator; cardiant; virucide;
 KW antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose;
 KW tumour; allergy; inflammation; autoimmune disease; circulatory system;
 KW viral; bacterial; infection; CCR4.

OS Mus musculus.
 XX WO2003084569-A1.
 PN 16-OCT-2003.

PD 09-APR-2003; 2003WO-JP004503.
 PF 09-APR-2002; 2002JP-00106949.

PR (KYOW) KYOWA HAKKO KOGYO KK.
 PA Niwa R, Shitara K;
 PI WPI: 2003-812676/76.

DR N-PSDB; ADF60652.
 XX Drugs containing antibody compositions produced by cells tolerant to
 PT lectin recognizing specific sugar-chain structure, useful in screening
 PT and treating patients not suitable for drugs not derived from these
 PT cells.

XX Disclosure; SEQ ID NO 13; 157pp; Japanese.
 PS The invention relates to a drug containing as the active ingredient, an
 CC antibody composition produced by cells tolerant to a lectin recognising a
 CC sugar-chain structure in which an alpha-bond is formed between the 6-
 CC position of N-acetylglucosamine at the reducing end of an N-glycoside
 CC bond-type complex sugar chain and the 1-position of fucose. The drugs are
 CC useful in screening and treating patients not suitable for drugs not
 CC derived from these cells. They are particularly useful as diagnostics,
 CC preventives or remedies for diseases accompanying tumour, allergy or
 CC inflammation, autoimmune diseases, diseases of the circulatory system,
 CC and viral or bacterial infections. In a method from the invention, a CCR4
 CC gene was used for constructing a vector (CAG-CCR4/pcDNA3) for producing a
 CC transfectant EL-4 cell (ATCC TIB-39) to express chimeric CCR4. Antibody-
 CC dependent cytotoxicity of the thus produced antibody composition was
 CC confirmed. The current sequence represents a protein related to the
 CC invention.

XX Sequence 140 AA;
 Query Match 85.8%; Score 533.5; DB 7; Length 140;
 Best Local Similarity 83.5%; Pred. No. 1e-37;
 Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOQPGAEIVKPGASVMSCKASGYTFTSYIHWIKOTPGGLEWIGAIYPNGDTSY 60
 Db 20 QVLOQPGAEIVKPGASVMSCKASGYTFTSYIHWIKOTPGGLEWIGAIYPNGDTSY 79
 QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSSAVYICARSTYYGDDWYFNWVGAGTTVTVS 139
Qy 118 S 118
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSSAVYICAREVRLR---YFDVWGAGTTVTVS 117
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSSAVYICARSTYYGDDWYFNWVGAGTTVTVS 139
Qy 118 S 118
Db 140 A 140

Search completed: May 9, 2006, 01:25:28
Job time : 107.251 secs

Query Match 85.8%; Score 533.5; DB 8; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTPGGLEWVGVIYFGNDISY 60
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYNNHWVKQTPGRGLEWIGAIYFGNGDTSY 79

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.8788 Seconds
(without alignments)
635.031 Million cell updates/sec

Title: US-10-700-632-7
Perfect score: 622
Sequence: 1 QVQLQQPGAEVVKPGASVKM.....EVLRLYFDVWVGAGTTVTSS 118
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	494	79.4	120	2 B22769	Ig heavy chain V r
2	491.5	79.0	119	2 PL0089	Ig heavy chain V r
3	484	77.8	118	2 S38717	Ig heavy chain V r
4	483	77.7	120	2 G28195	Ig heavy chain V r
5	481.5	77.4	138	2 E32513	Ig heavy chain pre
6	480.5	77.3	120	2 S25175	Ig heavy chain V r
7	480.5	77.3	136	2 PL0208	Ig heavy chain pre
8	479.5	77.1	117	1 MHMS75	Ig heavy chain V r
9	477.5	76.8	138	2 S21810	Ig heavy chain V r
10	476	76.5	101	2 S42184	Ig gamma chain V r
11	476	76.5	101	2 S42180	Ig gamma chain V r
12	476	76.5	102	2 S42180	Ig gamma chain V r
13	475	76.4	115	2 A54378	Ig heavy chain V r
14	473.5	76.1	117	1 MHMS4E	Ig heavy chain V r
15	473.5	76.1	140	2 T01407	Ig heavy chain (my
16	473	76.0	120	2 F28195	Ig heavy chain V r
17	471	75.7	115	2 C27563	Ig heavy chain V r
18	469	75.4	131	2 S66537	Ig heavy chain V r
19	468.5	75.3	123	2 S20646	Ig heavy chain V r
20	468	75.2	139	1 MHMS18	Ig heavy chain pre
21	468	75.2	287	4 PC4402	peIB leader/Ig hea
22	466	74.9	116	2 S53751	antibody Fab Jel 1
23	466	74.9	135	2 A30577	Ig heavy chain pre
24	465	74.8	133	2 PC1155	Ig heavy chain pre
25	464.5	74.7	246	2 S38950	Ig gamma chain - m
26	464.5	74.7	446	2 S40295	Ig gamma-2a chain
27	464	74.6	120	2 S41394	Ig heavy chain V r
28	464	74.6	141	2 A39276	Ig heavy chain pre
29	462	74.3	137	1 G2M543	Ig heavy chain pre

ALIGNMENTS

RESULT 1

B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)

C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C;Accession: B22769
R;Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A;Reference number: A90971; MUID:84236026; PMID:7188353
A;Accession: B22769
A;Molecule type: protein
A;Residues: 1-120 <DIL>

A;Cross-references: UNIPARC:UPI0000176B76
A;Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V
A;Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 494; DB 2; Length 120;
Best Local Similarity 77.5%; Pred. No. 4.7e-37;
Matches 93; Conservative 11; Mismatches 14; Indels 2; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPCNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYHMHVVKQKPGQGLEWIGRIHPDSSTNY 60
Qy 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAYVYCAR--EVLRLYFDVWVGAGTTVTSS 118
Db 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAYVYCARVYDYGSSYFDYWGQGTTLTVSS 120

RESULT 2

PL0089
Ig heavy chain V region (12S18-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
C;Accession: PL0089
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; J. Exp. Med. 169, 519-533, 1989

A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s ar
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0089
A;Molecule type: mRNA
A;Residues: 1-119 <MEE>
A;Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:G51591; PIDN:CAA41
A;Note: the sequences shown here is from the VH region of an antiidiotypic monoclonal an
A;Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical to
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Eur. J. Immunol. 23: 2503-2510, 1993
 A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe-
 A;Reference number: S42176; MUID:94009207; PMID:7691608
 A;Accession: S42179
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-101 <NOJ>
 A;Cross-references: UNIPARC:UPI00011655F; EMBL:Z25447; NID:g407816; PIDN:CAAB0934.1; P
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 476; DB 2; Length 101;
Best Local Similarity 90.7%; Pred. No. 1.6e-35;
Matches 88; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61
DB 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61

QY 62 QKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR 98
DB 62 QKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR 98

RESULT 12
S42180
Ig gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42180
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with speed
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42180
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <MOJ>
A:Cross-references: UNIPARC:UPI0000116561; EMBL:225449; NID:G407818; PIDN:CAA80936.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 476; DB 2; Length 102;
Best Local Similarity 90.7%; Pred. No. 1.6e-35;
Matches 88; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61
DB 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61

QY 62 QKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR 98
DB 62 QKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR 98

RESULT 13
A54378
Ig heavy chain V region anti-triplex DNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A54378
R:Agarie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc
A:Reference number: A54378; MUID:94165109; PMID:7509814
A:Accession: A54378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <AGA>
A:Cross-references: UNIPARC:UPI0000176E3F; GB:S68981; NID:G545744; PIDN:AAB30095.1; PID:
A:Experimental source: spleen and myeloma cell line MOPC 315.43
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:144172, NCBI:144173)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 475; DB 2; Length 115;
Best Local Similarity 75.7%; Pred. No. 2.2e-35;
Matches 87; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 1 EVLQQSGPELVKPGASVRIISKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGTKY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYFDVWGAGTTVT 115
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSSGGVLYGYWGGTTLT 115

RESULT 14
MMS4E
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1979 #sequence_revision 14-Nov-1993 #text_change 09-Jul-2004
C:Accession: A02039
R:Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A:Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain c
A:Reference number: A02039; MUID:83075344; PMID:6816276
A:Accession: A02039
A:Molecule type: protein
A:Residues: 1-117 <KEH>
A:Cross-references: UNIPROT:P01756; UNIPARC:UPI00000270F1
C:Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Diulfide bonds: #status predicted
F:55/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match 76.1%; Score 473.5; DB 1; Length 117;
Best Local Similarity 77.1%; Pred. No. 3e-35;
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 1 EVLQQSGPELVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGTTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYFDVWGAGTTVTSS 118
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARDYDW-YFDVWGAGTTVTSS 117

RESULT 15
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T01407
R:Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamanot
Microbiol. Immunol. 36, 855-863, 1992
A:Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A:Reference number: Z14317; MUID:93116638; PMID:1474935
A:Accession: T01407
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <TAK>
A:Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:G262657
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 76.1%; Score 473.5; DB 2; Length 140;
Best Local Similarity 77.1%; Pred. No. 3.6e-35;
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 20 EVLQQSGPELVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGTTSY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYFDVWGAGTTVTSS 118
DB 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARDYDW-YFDVWGAGTTVTSS 136

Search completed: May 9, 2006, 01:33:51
Job time : 18.8788 secs

THIS PAGE BLANK (uspto)

DT 01-DEC-2001 (TREMBlRel. 19, C

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonym=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX -x311_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSP; P01751; IAGW.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
FT SEQUENCE 143 AA; 15775 MW; 918C6012B44EFEBP CRC64;

Query Match 79.6%; Score 495; DB 2; Length 143;
Best Local Similarity 78.8%; Pred. No. 9.6e-45;
Matches 93; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGQGLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGQGLEWVGVIYPGNDISY 60
QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLRYFDVVGAGTTVTVSS 118
Db 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLRYFDVVGAGTTVTVSS 118

RESULT 3
Q924Q0_MOUSE
ID Q924Q0_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbett S., Hirn M., Roth C., These J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the CAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784 (1988).
DR EMBL; AB067795; BAB63280.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSP; P01751; IAGW.
DR SMR; Q924Q0; 1-134.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
FT SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Q924Q0_MOUSE
ID Q924Q0_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE V165-D-J-C mu protein (Fragment).
GN Name=V165-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069915; BAB63931.1; -; mRNA.
DR PIR; PH1159; PH1159.
DR HSP; P01751; IAGW.
DR SMR; Q924Q0; 1-134.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
FT SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

```

```
Query Match 78.6%; Score 489; DB 2; Length 143;
Best Local Similarity 77.1%; Pred. No. 4.2e-44;
Matches 91; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPCNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPCNDISY 60
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTSS 118
DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTSS 118

RESULT 5
Q8VCX7 MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2464031;
RA Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";
RL J. Immunol. 142:888-893(1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.

QY GO:0003823; F:antigen binding; IDA.
QY GO:0005515; F:protein binding; IPI.
QY GO:0004888; F:transmembrane receptor activity; IDA.
QY GO:0000187; P:activation of MAPK activity; IDA.
QY GO:0030333; P:antigen processing; IDA.
QY GO:0005053; P:B cell receptor signaling pathway; IDA.
QY GO:0045022; P:early endosome to late endosome transport; IDA.
QY GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
QY GO:0030890; P:positive regulation of B cell proliferation; IDA.
QY GO:0045807; P:positive regulation of endocytosis; IDA.
QY GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . ; IDA.
QY InterPro; IPR007110; Ig-like.
QY InterPro; IPR003597; Ig-cl.
QY InterPro; IPR003006; Ig_MHC.
QY InterPro; IPR003596; Ig_v.
QY Pfam; PF07654; C1-set; 4.
QY SMART; SM00406; IGV; 1.
QY PROSITE; PS00835; IG_LIKE; 5.
QY PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 77.8%; Score 484; DB 2; Length 613;
Best Local Similarity 76.3%; Pred. No. 8e-43;
Matches 90; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPCNDISY 60
DB 20 QVQLQSGAEVVKPGASVKISCKATGYTSSWIEWVKRPGHGLEWIGELPGSGSTNY 79
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTSS 118
DB 80 NEKFKGKATFTADTSSNTAYMQLSSLTSDSAVYVCARRLGRWYFDVWGAGTTVTSS 137

RESULT 6
HV13 MOUSE STANDARD; PRT; 117 AA.
ID HV13 MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS; The sequences of 10 hybridoma proteins that also
bind dextran differ from that shown at 1-7 positions, many of
which occur in the D and J segments.
CC -!- MISCELLANEOUS; This protein binds dextran.
CC -!- SIMILARITY; Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC PIR; A26242; MHMSJ5.
CC HSSP; P01751; 1NOB.
CC SMR; P01757; 1-117.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
```

```

DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;

Query Match 77.1%; Score 479.5; DB 1; Length 117;
Best Local Similarity 78.0%; Pred. No. 3.4e-43;
Matches 92; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTQCGLEWGVYIPGNDLISY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWKVQSHGKSLIEWIGDINPNNGGTSY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTSS 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYYCARD-RWYFDVWGAGTTVTSS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q7TMK1 MOUSE
ID Q7TMK1 MOUSE PRELIMINARY; PRT; 470 AA.
AC Q7TMK1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAHS5910.1; -; mRNA.
DR HSSP; P01865; 1KBS.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.

```

```

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51728 MW; 6D90E4DF896BB090 CRC64;

Query Match 77.1%; Score 479.5; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 1.8e-42;
Matches 90; Conservative 13; Mismatches 15; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTQCGLEWGVYIPGNDLISY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 EVQLQQSGPELVKPGASVKMSCKASGYTFTGYIHWIKQSHGKSLIEWIGLVNPNNGDTSY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAR---EVRLRYFDVWGAGTTVTVS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   |
DB 140 S 140

RESULT 8
Q924R7 MOUSE
ID Q924R7 MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924R7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067782; BAB63267.1; -; mRNA.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R7; 1-134.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

```



```
Query Match      77.0%; Score 479; DB 2; Length 143;
Best Local Similarity 75.4%; Pred. No. 4.9e-43;
Matches 89; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKLSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYPGNDISY 60
Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAREVRLRYFDVWGAGTTVTSS 118
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCAREVRLRYFDVWGAGTTVTSS 118

RESULT 9
Q924R3 MOUSE
ID Q924R3 MOUSE PRELIMINARY; PRT; 145 AA.
AC Q924R3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAR idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3211160;
RA Kaartinen M., Rocca-Serra J., Makela O.;
RT "Combinatorial association of V genes: one VH gene codes for three
RT non-cross-reactive monoclonal antibodies each specific for a different
RT antigen (phoxalone, NP or gat).";
RL Mol. Immunol. 25:859-865(1988).
DR EMBL; AB067787; BAB63272.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; J00078; J00078.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
```

```
PIR; S26744; S26744.
DR HSP; P01751; 1A6W.
DR SNR; Q924R3; 1-136.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36B4280BA81 CRC64;

Query Match      76.5%; Score 476; DB 2; Length 145;
Best Local Similarity 75.8%; Pred. No. 1e-42;
Matches 91; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKLSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYPGNDISY 60
Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAREV--RLRYFDVWGAGTTVTSS 118
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCAREVLDGNWYFDVWGAGTTVTSS 120

RESULT 10
Q924R8 MOUSE
ID Q924R8 MOUSE PRELIMINARY; PRT; 146 AA.
AC Q924R8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAR idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB067781; BAB63266.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
```

```
DR PIR; PH1153; PH1153.
DR HSP; P01751; 1A6W.
DR SMR; Q924R8; 1-137.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1DF1B7538 CRC64;

Query Match 76.4%; Score 475.5; DB 2; Length 146;
Best Local Similarity 74.4%; Pred. No. 1.2e-42;
Matches 90; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
DB 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREV---RLRYFDVWGAGTTVTVS 117
DB 61 NEKFSKATLTVDKPSSTAYMQLSLTSDSAVYVCARSYGLYPDYWGQGTTLTVS 120
QY 118 S 118
DB 121 S 121

RESULT 11
Q91VA2 MOUSE
ID Q91VA2 MOUSE PRELIMINARY; PRT; 143 AA.
AC Q91VA2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kozono Y., Kozono H., Azuma T.;
RC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB067786; BAB63271.1; -; mRNA.
DR EMBL; AB069911; BAB63927.1; -; mRNA.
DR PIR; PH1105; PH1105.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR HSP; P01751; 1A6W.
DR SMR; Q91VA2; 1-134.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143

SQ SEQUENCE 143 AA; 15617 MW; 51952152F6F3AD47 CRC64;

Query Match 76.2%; Score 474; DB 2; Length 143;
Best Local Similarity 74.6%; Pred. No. 1.7e-42;
Matches 88; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
DB 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118
DB 61 NEKFSKATLTVDKPSSTAYMQLSLTSDSAVYVCARSYGVADVWGTTVTVS 118

RESULT 12
HV12 MOUSE
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
EX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC protein has also been determined.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A02039; MHMS4E.
DR HSP; P01751; 1NOB.
DR SMR; P01756; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT CARBOHYD 55 55 N-linked (GlcNAc..) (complex).
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BB447E41 CRC64;

Query Match 76.1%; Score 473.5; DB 1; Length 117;
Best Local Similarity 77.1%; Pred. No. 1.5e-42;
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
DB 1 EVLOQSGPELVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWGVYIPGNDISY 60
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118
DB 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYVCARDYDW-YFDVWGAGTTVTVS 117
```

```

RESULT 13
Q5BJZ2_RAT PRELIMINARY; PRT; 458 AA.
AC Q5BJZ2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AAH91272.1; -; mRNA.
DR SNR; Q5BJZ2; 21-454.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 76.08; Score 472.5; DB 2; Length 458;
Best Local Similarity 76.08; Pred. No. 9.6e-42;
Matches 92; Conservative 9; Mismatches 13; Indels 7; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKSCASGYTFTSYTHWIKOTPGGLEWGVVYPCNDISY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 20 QVQLQSGAEVLPFGSSVKISCRASGYTFYTHWIKQPGNGLEWGIWYFGNGTKY 79
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTSS 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 80 NQKFNKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD----YFDGYDWGQGVMTVS 135
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

```

```

QY 118 S 118
DB 136 S 136

RESULT 14
Q921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells.";
RMol. Immunol. 34:441-452 (1997).
DR EMBL; U79801; AAD00293.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SNR; Q921C4; 1-118.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EBC559D31EC4FC CRC64;

Query Match 75.98; Score 472; DB 2; Length 118;
Best Local Similarity 73.78; Pred. No. 2.2e-42;
Matches 87; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKSCASGYTFTSYTHWIKOTPGGLEWGVVYPCNDISY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 1 QVQVQSGAEVLPFGSSVKISCRASGYTFYTHWIKQPGNGLEWGIWYFGNGTYS 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTSS 118
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 61 TQKFRGKATLTADKSSSTAYMQLSSLTSDSAVYVCARRVGGYFDVWGQGTTLTVSS 118
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 15
Q924P5_MOUSE PRELIMINARY; PRT; 144 AA.
AC Q924P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

```


GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 26.5628 Seconds
(without alignments)
367.271 Million cell updates/sec

Title: US-10-700-632-7
Perfect score: 622
Sequence: 1 QVQLQPGAEVVRKPGASVKM.....EVLRLYFDVWGAGTTVTYSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	85.8	140	2	US-08-475-815B-11
2	533.5	85.8	470	2	US-09-238-741-4
3	525.5	84.5	140	1	US-08-476-275-6
4	525.5	84.5	140	2	US-08-475-813-6
5	510.5	82.1	121	2	US-08-579-378A-7
6	510.5	82.1	121	4	PCT-US93-11612-7
7	510.5	82.1	140	4	PCT-US93-11612-4
8	503	80.9	140	2	US-09-724-138-44
9	503	80.9	140	2	US-09-630-198-44
10	502.5	80.8	140	2	US-08-579-378A-4
11	501	80.5	257	2	US-09-419-788-113
12	500	80.4	118	2	US-08-766-350B-48
13	493	79.3	273	1	US-08-403-853-18
14	488.5	78.5	135	1	US-08-860-174A-4
15	488.5	78.5	274	1	US-08-860-174A-12
16	479.5	77.1	119	1	US-10-194-975-121
17	478.5	76.9	119	1	US-08-553-497A-12
18	477.5	76.8	117	2	US-09-157-370-2
19	476.5	76.6	288	2	US-09-423-439-38
20	476.5	76.6	673	2	US-09-423-439-32
21	475.5	76.4	119	2	US-08-881-037-60
22	472.5	76.0	119	2	US-08-767-128-10
23	472.5	76.0	445	1	US-08-353-400-33
24	472.5	76.0	464	1	US-08-353-400-36
25	471.5	75.8	119	2	US-08-881-037-62
26	471	75.7	117	2	US-09-065-059-15
27	471	75.7	117	2	US-08-913-555-15

28	471	75.7	269	1	US-08-428-257A-72	Sequence 72, Appl
29	471	75.7	269	1	US-08-491-988-3	Sequence 3, Appli
30	471	75.7	402	1	US-08-491-988-9	Sequence 9, Appli
31	471	75.7	415	1	US-08-491-988-7	Sequence 7, Appli
32	471	75.7	435	1	US-08-491-988-5	Sequence 5, Appli
33	470.5	75.6	119	2	US-08-881-037-63	Sequence 63, Appl
34	470	75.6	122	1	US-08-236-520-9	Sequence 9, Appli
35	470	75.6	122	4	PCT-US95-05262-9	Sequence 9, Appli
36	469.5	75.5	143	4	PCT-US95-05262-7	Sequence 7, Appli
37	469.5	75.5	143	4	PCT-US95-05262-7	Sequence 7, Appli
38	468.5	75.2	140	1	US-07-946-421-24	Sequence 24, Appl
39	468	75.2	114	2	US-09-344-587-10	Sequence 10, Appl
40	468	75.2	122	2	US-10-092-246-10	Sequence 10, Appl
41	468	75.2	122	2	US-10-092-246-11	Sequence 10, Appl
42	468	75.2	122	2	US-10-096-246A-10	Sequence 10, Appl
43	468	75.2	122	2	US-10-096-246A-11	Sequence 11, Appl
44	467.5	75.2	117	2	US-08-913-555-27	Sequence 27, Appl
45	467.5	75.2	119	2	US-08-881-037-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-475-815B-11
; Sequence 11, Application US/08475815B
; Patent No. 6399061
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIO-LABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; NUMBER OF SEQUENCES: 11
; TITLE OF INVENTION: LYMPHOMA
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
US-08-475-815B-11

Query Match      85.8%; Score 533.5; DB 2; Length 140;
Best Local Similarity 83.5%; Pred. No. 1.8e-42;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOQPAGAEVVKPGASVMSCKASGYTFTSYIIHWIKQTPQGGLWGVVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVLOQPGAEVLKPGASVMSCKASGYTFTSYNMHWKQTPGRLGIEWIGAIYPGNGDTSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARTSYGGDWYFNWVGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 2
US-09-238-741-4
; Sequence 4, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238,741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match      85.8%; Score 533.5; DB 2; Length 470;
Best Local Similarity 83.5%; Pred. No. 6.5e-42;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOQPAGAEVVKPGASVMSCKASGYTFTSYIIHWIKQTPQGGLWGVVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVLOQPGAEVLKPGASVMSCKASGYTFTSYNMHWKQTPGRLGIEWIGAIYPGNGDTSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARTSYGGDWYFNWVGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 3
US-08-476-275-6
; Sequence 6, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
```

```

; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
; TITLE OF INVENTION: Lymphoma
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-275-6

Query Match      84.5%; Score 525.5; DB 1; Length 140;
Best Local Similarity 82.6%; Pred. No. 9.8e-42;
Matches 100; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPAGAEVVKPGASVMSCKASGYTFTSYIIHWIKQTPQGGLWGVVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVLOQPGAEVLKAGASVMSCKASGYTFTSYNMHWKQTPGRLGIEWIGAIYPGNGDTSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARSTYGGDWYFNWVGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 4
US-08-475-813-6
; Sequence 6, Application US/08475813
; Patent No. 6682734
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
```


Db 140 S 140

RESULT 9

US-09-630-198-44

Sequence 44, Application US/09630198

Patent No. 6893625

GENERAL INFORMATION:

APPLICANT: Robinson, Randy

APPLICANT: Liu, Alvin

APPLICANT: Ledbetter, Jeffrey

TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Antigen

FILE REFERENCE: PPL-001CN

CURRENT APPLICATION NUMBER: US/09/630,198

CURRENT FILING DATE: 2000-08-01

PRIOR FILING DATE: US 09/021934

PRIOR FILING DATE: 1998-02-12

PRIOR APPLICATION NUMBER: US 08/471984

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 07/665939

PRIOR FILING DATE: 1991-03-05

PRIOR APPLICATION NUMBER: US 07/195961

PRIOR FILING DATE: 1988-05-13

PRIOR APPLICATION NUMBER: US 07/016202

PRIOR FILING DATE: 1987-01-08

PRIOR APPLICATION NUMBER: PCT/US86/02269

PRIOR FILING DATE: 1986-10-27

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn version 3.0

SEQ ID NO 44

LENGTH: 140

TYPE: PRT

ORGANISM: Mus musculus

US-09-630-198-44

Query Match 80.9%; Score 503; DB 2; Length 140;

Best Local Similarity 79.3%; Pred. No. 1.2e-39;

Matches 96; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYFGNDISY 60

Db 20 QAYLQSGAEIVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQLEWIGAIYFGNDTSY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVMGAGTTVTY 116

Db 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVYVYNSYWFYDVMGTGTTVY 139

QY 117 S 117

Db 140 S 140

RESULT 10

US-08-579-378A-4

Sequence 4, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:

APPLICANT: Co. Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

Db 140 S 140

US-08-579-378A-4

Query Match 80.8%; Score 502.5; DB 2; Length 140;

Best Local Similarity 78.5%; Pred. No. 1.4e-39;

Matches 95; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYFGNDISY 60

Db 20 EVQLQSGDPLVKPGASVKMSCKASGYTFTSYNMHWVKQKPGQLEWIGVIYYPNDGTKY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREV---RLRYFDVMGAGTTVTYS 117

Db 80 NQKFKGKATLTDSKSSSTAYMQLSSLTSDSAVYVCAREYGNVYRVFDMVGAGTTVTYS 139

QY 118 S 118

Db 140 S 140

RESULT 11

US-09-419-788-113

Sequence 113, Application US/09419788

Patent No. 6825325

GENERAL INFORMATION:

APPLICANT: FISCHER, Rainer

APPLICANT: SCHILLBERG, Stefan

APPLICANT: NAHRING, Jorg

APPLICANT: SACK, Markus

APPLICANT: MONECKE, Michael

APPLICANT: LIAO, Yu-Cal

APPLICANT: SPIEGEL, Holger

APPLICANT: ZIMMERMAN, Sabine

APPLICANT: EMANS, Neil

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Resistance

FILE REFERENCE: 0147-0189P

CURRENT APPLICATION NUMBER: US/09/419,788

CURRENT FILING DATE: 1999-10-18

EARLIER APPLICATION NUMBER: 98 11 9630.6 EP

EARLIER FILING DATE: 1998-10-16

EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA

EARLIER FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 163

SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-113

Query Match      80.5%; Score 501; DB 2; Length 257;
Best Local Similarity 80.5%; Pred. No. 3.6e-39;
Matches 95; Conservative 9; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVMGAGTTVTV 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCARP-----DVMGAGTLLTV 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-08-766-350B-48
; Sequence 48, Application US/08766350B
; Patent No. 6949244
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malay A
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,350B
; FILING DATE: 13-Dec-1996
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-766-350B-48

Query Match      80.4%; Score 500; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 1.9e-39;
Matches 93; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

; SEQ ID NO 117
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-08-403-853-18

Query Match      79.3%; Score 493; DB 1; Length 273;
Best Local Similarity 78.5%; Pred. No. 2.2e-38;
Matches 95; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPQGLEWGVVYFGNDISY 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCARE-VRLRY---FDVMGAGTTVT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 NQKPKGKATLTADKSSNTAYMQLSLTSDSAVYYCARSGGSYRVDGDFYWGQGT 142
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 S 117

```


THIS PAGE BLANK (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 88.6277 Seconds
(without alignments)

556.303 Million cell updates/sec

Title: US-10-700-632-7

Perfect score: 622

Sequence: 1 QVQLQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTTVTYSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	100.0	118	5	US-10-700-632-7
2	618	99.4	117	5	US-10-700-632-73
3	613	98.6	118	5	US-10-700-632-9
4	536.5	86.3	121	4	US-10-366-709-39
5	534.5	85.9	412	4	US-10-013-173-6
6	534.5	85.9	412	4	US-10-150-762-6
7	534.5	85.9	412	4	US-10-244-821-6
8	533.5	85.8	140	4	US-10-238-681-11
9	533.5	85.8	140	4	US-10-411-037-62
10	533.5	85.8	140	4	US-10-411-026-62
11	533.5	85.8	140	4	US-10-410-962-62
12	533.5	85.8	140	4	US-10-411-049-62
13	533.5	85.8	140	4	US-10-327-663-14
14	533.5	85.8	140	4	US-10-410-930-62
15	533.5	85.8	140	4	US-10-410-997-62
16	533.5	85.8	140	4	US-10-411-012-62
17	533.5	85.8	140	4	US-10-287-994-62
18	533.5	85.8	140	4	US-10-410-913-62
19	533.5	85.8	140	5	US-10-723-003-36
20	533.5	85.8	140	5	US-10-410-980-62
21	533.5	85.8	140	5	US-10-410-897-62
22	533.5	85.8	140	5	US-10-492-261-62
23	533.5	85.8	140	6	US-11-004-639-36
24	533.5	85.8	368	5	US-10-880-028-47
25	533.5	85.8	368	5	US-10-880-320-47
26	533.5	85.8	451	5	US-10-822-231-4
27	533.5	85.8	451	5	US-10-822-231-5

28	533.5	85.8	470	5	US-10-723-003-40	Sequence 40, Appl
29	533.5	85.8	470	6	US-11-019-180-4	Sequence 4, Appl
30	533.5	85.8	470	6	US-11-004-639-40	Sequence 40, Appl
31	533.5	85.8	626	5	US-10-723-003-44	Sequence 44, Appl
32	533.5	85.8	626	6	US-11-004-639-44	Sequence 44, Appl
33	533.5	85.8	641	5	US-10-723-003-46	Sequence 46, Appl
34	533.5	85.8	641	6	US-11-004-639-46	Sequence 46, Appl
35	533.5	85.8	657	5	US-10-723-003-48	Sequence 48, Appl
36	533.5	85.8	657	6	US-11-004-639-48	Sequence 48, Appl
37	531.5	85.5	120	4	US-10-366-709-35	Sequence 35, Appl
38	530.5	85.3	423	4	US/10/013	Sequence 8, Appl
39	530.5	85.3	423	4	US/10/150	Sequence 8, Appl
40	530.5	85.3	423	4	US/10/244	Sequence 8, Appl
41	526.5	84.6	121	5	US-10-917-599-1	Sequence 1, Appl
42	525.5	84.5	140	3	US-09-905-928-6	Sequence 6, Appl
43	525.5	84.5	140	4	US-10-096-964-6	Sequence 6, Appl
44	525.5	84.5	140	5	US-10-956-039-6	Sequence 6, Appl
45	521	83.8	122	5	US-10-917-599-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-10-700-632-7

; Sequence 7, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 7

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-700-632-7

Query Match 100.0%; Score 622; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 7.7e-49;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDISY 60

Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDISY 60

Qy 61 NQPKGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGAGTTVTYSS 118

Db 61 NQPKGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGAGTTVTYSS 118

RESULT 2

US-10-700-632-73

; Sequence 73, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 73

```
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73

Query Match      99.4%; Score 618; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 117
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 117

RESULT 3
US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE OF INVENTION: LEUKEMIA USING THE SAME
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9

Query Match      98.6%; Score 613; DB 5; Length 118;
Best Local Similarity 98.3%; Pred. No. 5.1e-48;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118

RESULT 4
US-10-366-709-39
; Sequence 39, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 39
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain CA20VH amino acid sequence
US-10-366-709-39

Query Match      86.3%; Score 536.5; DB 4; Length 121;
Best Local Similarity 84.3%; Pred. No. 4.6e-41;
Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 120

QY 118 S 118
Db 121 S 121

RESULT 5
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
US-10-013-173-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 128 QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWIGAIYFGNGDTSY 187

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTV 116
Db 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTV 246

QY 117 SS 118
Db 247 SS 248

RESULT 6
US-10-150-762-6
; Sequence 6, Application US/10150762
```

```

; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
; US-10-150-762-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWKQTTPGQGLEWVGVIYFGNDDISY 60
DB 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGQGLEWIGAIYFGNGDTSY 187

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 116
DB 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 246

QY 117 SS 118
DB 247 SS 248

RESULT 7
US-10-244-821-6
; Sequence 6, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
; US-10-244-821-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

```

```

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWKQTTPGQGLEWVGVIYFGNDDISY 60
DB 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGQGLEWIGAIYFGNGDTSY 187

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 116
DB 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 246

QY 117 SS 118
DB 247 SS 248

RESULT 8
US-10-238-681-11
; Sequence 11, Application US/10238681
; Publication No. US20030147885A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED
; ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; FILE REFERENCE: 37003/0291808
; CURRENT APPLICATION NUMBER: US/10/238,681
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 08/921,060
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/149,099
; PRIOR FILING DATE: 1993-11-03
; PRIOR APPLICATION NUMBER: 07/978,891
; PRIOR FILING DATE: 1992-11-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Murine sp.
; US-10-238-681-11

Query Match      85.8%; Score 533.5; DB 4; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-40;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

```

```

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWKQTTPGQGLEWVGVIYFGNDDISY 60
DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGQGLEWIGAIYFGNGDTSY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 117
DB 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 139

QY 118 S 118
DB 140 A 140

RESULT 9
US-10-411-037-62
; Sequence 62, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David

```

RESULT 10
US-10-411-026-62
; Sequence 62, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249

Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79
QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139

QY 118 S 118

Db 140 A 140

RESULT 12

US-10-411-049-62

; Sequence 62, Application US/10411049

; Publication No. US20040082026A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DePrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; APPLICANT: Bove, Caryn

; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON

; FILE REFERENCE: 040853-01-5055

; CURRENT APPLICATION NUMBER: US/10/411,049

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 62

; LENGTH: 140

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-411-049-62

Query Match 85.8%; Score 533.5; DB 4; Length 140;

Best Local Similarity 83.5%; Pred. No. 1e-40;

Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 60
Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79

QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139

QY 118 S 118

Db 140 A 140

RESULT 13

US-10-327-663-14

; Sequence 14, Application US/10327663

; Publication No. US20040093621A1

; GENERAL INFORMATION:

; APPLICANT: Kenya SHITARA

; APPLICANT: Mikiko SAKURADA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohisa SHINKAWA
; APPLICANT: Mitsuo SATOH
; APPLICANT: RYOSUKE NAKANO
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
; FILE REFERENCE: 249-289
; CURRENT APPLICATION NUMBER: US/10/327,663
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: JP 2001-392753
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JP 2002-106948
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: JP 2002-319975
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-327-663-14

Query Match 85.8%; Score 533.5; DB 4; Length 140;

Best Local Similarity 83.5%; Pred. No. 1e-40;

Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 60
Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79

QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139

QY 118 S 118

Db 140 A 140

RESULT 14

US-10-410-930-62

; Sequence 62, Application US/10410930

; Publication No. US20040115168A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DePrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; APPLICANT: Bove, Caryn

; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON

; FILE REFERENCE: 040853-01-5056

; CURRENT APPLICATION NUMBER: US/10/410,930

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	536.5	86.3	121	11	US-11-107-028-35		Sequence 35, Appl
2	533.5	85.8	140	10	US-11-183-218-62		Sequence 62, Appl
3	533.5	85.8	140	11	US-11-183-205-62		Sequence 62, Appl
4	533.5	85.8	451	11	US-11-124-620-5		Sequence 7, Appl
5	533.5	85.8	451	11	US-11-124-620-7		Sequence 7, Appl
6	533.5	85.8	451	11	US-11-208-422-25		Sequence 25, Appl
7	507	81.5	122	10	US-11-254-182-28		Sequence 28, Appl
8	507	81.5	122	11	US-11-120-338-7		Sequence 7, Appl
9	507	81.5	122	11	US-11-106-820-7		Sequence 7, Appl
10	507	81.5	122	11	US-11-143-077-7		Sequence 7, Appl
11	507	81.5	122	11	US-11-190-364-7		Sequence 7, Appl
12	507	81.5	122	11	US-11-147-780-7		Sequence 7, Appl
13	507	81.5	122	11	US-11-143-386-7		Sequence 7, Appl
14	507	81.5	122	11	US-11-187-364-7		Sequence 7, Appl
15	507	81.5	253	11	US-11-106-820-20		Sequence 20, Appl
16	507	81.5	253	11	US-11-190-364-18		Sequence 18, Appl
17	507	81.5	253	11	US-11-147-780-18		Sequence 18, Appl
18	503	80.9	121	11	US-11-107-028-27		Sequence 27, Appl
19	500	80.4	118	11	US-11-126-798-48		Sequence 48, Appl
20	492.5	79.2	121	11	US-11-107-028-37		Sequence 37, Appl
21	492	79.1	122	11	US-11-107-028-39		Sequence 39, Appl

```
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-218-62
```

```
Query Match      85.8%; Score 533.5; DB 10; Length 140;
Best Local Similarity 83.5%; Pred. No. 6.9e-38;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGLEWVGVIYPGNDDISY 60
Db      20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGLEWIGAIYPGNGDTSY 79

QY      61 NQKPKGKATLTADKSSSTTAYMQLSLSLTSSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
Db      80 NQKPKGKATLTADKSSSTTAYMQLSLSLTSSEDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139

QY      118 S 118
Db      140 A 140
```

```
RESULT 3
US-11-183-205-62
; Sequence 62, Application US/11183205
; Publication No. US2006030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
```

```
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-205-62

Query Match      85.8%; Score 533.5; DB 11; Length 140;
Best Local Similarity 83.5%; Pred. No. 6.9e-38;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPOGLEWVGVIYPGNDDISY 60
Db      20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGLEWIGAIYPGNGDTSY 79

QY      61 NQKPKGKATLTADKSSSTTAYMQLSLSLTSSEDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
Db      80 NQKPKGKATLTADKSSSTTAYMQLSLSLTSSEDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139

QY      118 S 118
Db      140 A 140

RESULT 4
US-11-124-620-5
; Sequence 5, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
```

;; PRIOR FILING DATE: 2004-03-26
;; PRIOR APPLICATION NUMBER: US 10/672,280
;; PRIOR FILING DATE: 2003-09-26
;; PRIOR APPLICATION NUMBER: US 10/379,392
;; PRIOR FILING DATE: 2003-03-03
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 5
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Synthetic
;; NAME/KEY: misc feature
;; LOCATION: (243)..(243)
;; OTHER INFORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
;; OTHER INFORMATION: Glutamine or Threonine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (244)..(244)
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (268)..(268)
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (272)..(272)
;; OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (276)..(276)
;; OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (278)..(278)
;; OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (301)..(301)
;; OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (302)..(302)
;; OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (330)..(330)
;; OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (334)..(334)
;; OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (336)..(336)
;; OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine
;; OTHER INFORMATION: or Glutamine
US-11-124-620-5

Query Match 85.8%; Score 533.5; DB 11; Length 451;
Best Local Similarity 83.5%; Pred. No. 1.9e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60

Qy 61 NQPKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTTIVS 117
Db 61 NQPKFGKATLTADKSSSTAYMQLSLTSDSAVYICARSTYYGCDWYFNVWGAGTTTIVS 120

Qy 118 S 118
Db 121 A 121

RESULT 5
US-11-124-620-7
;; Sequence 7, Application US/11124620
;; Publication No. US20060024298A1
;; GENERAL INFORMATION:
;; APPLICANT: Lazar, Gregory Alan
;; APPLICANT: Dang, Wei
;; APPLICANT: Desjarlais, John R.
;; APPLICANT: Karki, Sher Bahadur
;; APPLICANT: Vafa, Omid
;; APPLICANT: Hayes, Robert
;; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
;; FILE REFERENCE: A-71386-9
;; CURRENT APPLICATION NUMBER: US/11/124,620
;; CURRENT FILING DATE: 2005-05-05
;; PRIOR APPLICATION NUMBER: US 60/568,440
;; PRIOR FILING DATE: 2004-07-15
;; PRIOR APPLICATION NUMBER: US 60/589,906
;; PRIOR FILING DATE: 2004-07-20
;; PRIOR APPLICATION NUMBER: US 60/627,026
;; PRIOR FILING DATE: 2004-11-09
;; PRIOR APPLICATION NUMBER: US 60/626,991
;; PRIOR FILING DATE: 2004-11-10
;; PRIOR APPLICATION NUMBER: US 60/627,774
;; PRIOR FILING DATE: 2004-11-12
;; PRIOR APPLICATION NUMBER: US 10/822,231
;; PRIOR FILING DATE: 2004-03-26
;; PRIOR APPLICATION NUMBER: US 10/672,280
;; PRIOR FILING DATE: 2003-09-26
;; PRIOR APPLICATION NUMBER: US 10/379,392
;; PRIOR FILING DATE: 2003-03-03
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 7
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-124-620-7

Query Match 85.8%; Score 533.5; DB 11; Length 451;
Best Local Similarity 83.5%; Pred. No. 1.9e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60

Qy 61 NQPKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTTIVS 117
Db 61 NQPKFGKATLTADKSSSTAYMQLSLTSDSAVYICARSTYYGCDWYFNVWGAGTTTIVS 120

RESULT 6
US-11-208-422-25
;; Sequence 25, Application US/11208422
;; Publication No. US20060067930A1
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camellia W.
;; APPLICANT: Lien, Samantha
;; APPLICANT: Lowman, Henry B.
;; APPLICANT: Marvin, Jonathan S.
;; APPLICANT: Meng, Yu-Ju G.
;; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
;; FILE REFERENCE: P2158R1


```

RESULT 10
US-11-143-077-7
; Sequence 7, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-077-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

RESULT 11
US-11-190-364-7
; Sequence 7, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-190-364-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAREVRLR-----YFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

RESULT 12
US-11-147-780-7
; Sequence 7, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-147-780-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAREVRLR-----YFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

RESULT 13
US-11-143-386-7
; Sequence 7, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAREVRLR-----YFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

```

```

DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120
QY 117 SS 118
DB 121 SS 122

RESULT 12
US-11-147-780-7
; Sequence 7, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-147-780-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAREVRLR-----YFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

RESULT 13
US-11-143-386-7
; Sequence 7, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYFGNDDISY 60
DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAREVRLR-----YFDVWGAGTTVTY 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYNSYNYFDVWGAGTTVTY 120

QY 117 SS 118
DB 121 SS 122

```

Qy	61	NQKFKGKATLTADKSGTAYMOLSLTSEDNAVYFCAREVRLR---	YFDVWGAGTTVTW	116
		:		
Db	61	NQKFKGKATLTVDKSGTAYMOLSLTSEDNAVYFCARVVYSNSWYFDDVWGAGTTVTW	120	
		:		
Qy	117	SS	118	
Db	121	SS	122	

RESULT 14

```

US-11-187-364-7
; Sequence 7, Application US/11187364
; Publication No. US2006062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitraya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-187-364-7

```

Query Match 81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

Qy	1	QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHIKQTQPGGLEWGVVYIPGNDISY	60
Db	1	QAYLQSGAEELVRPGASVKMSCKASGYTFTSYTHHWKQTQPGLEWIGAIYPGNGDTSY	60
Qy	61	NQKFKGKATLTADSKSTTAYMOLSLITSEDSAVVYCAREVRLR-----YFDVWGAGTGVTV	116
Db	61	NQKFKGKATLTVDKSSSTAYMOLSLITSEDSAVVYFCAVVYYSNYSWYFDWGTGTVTV	120

Qy	117	SS	118
Db	121	SS	122

RESULT 15

```

US-11-106-820-20
; Sequence 20, Application US/11106820
; Publication No. US2006002930A1
;
; GENERAL INFORMATION:
;
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
;
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 20
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-20

```

Query Match	81.5%	Score 507;	DB 11;	Length 253;
Best Local Similarity	79.5%;	Pred. No. 1.9e-35;		
Matches 97;	Conservative	7;	Mismatches 14;	Indels 4;
				Gaps 1;

QY	1	QVQLQQPGAEVVRPGCASVKMSCKASGYTFTSYIHWIKQTPTCGGLEWGVIIIPGNDNISY	60
Db	24	QAYLQOSGAELVRPGCASVKMSCKASGYTFTSYNMHWIKQTPTQGLEWIGAIYPGNGDTSY	83
QY	61	NQKPKGKATLTADKSSTTAYNQLSLLTSDSGAVYYCAREVRLR----	116
Db	84	NQKPKGKATLTADKSSTTAYNQLSLLTSDSGAVYYCAREVRLR----	143
QY	117	SS 118	
Db	144	SS 145	

Search completed: May 9, 2006, 02:05:58
Job time : 15.0476 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 101.749 Seconds
(without alignments)
487.964 Million cell updates/sec

Title: US-10-700-632-8
Perfect score: 581
Sequence: 1 NIMLTQSPSLAVSAGEKVT.....CHQYLSRTPGGGKLEIKR I13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	581	100.0	113	8 ADO32092	Ado32092 Mouse ant
2	581	100.0	114	8 ADO32146	Ado32146 Mouse ant
3	545	93.8	113	9 ADX37184	Adx37184 Murine SM
4	545	93.8	113	9 AEA88701	Aea88701 Mouse ant
5	545	93.8	133	9 ADV92466	Adv92466 Mouse SM5
6	545	93.8	133	9 ADV98529	Adv98529 Novel chi
7	545	93.8	239	9 ADV92470	Adv92470 SM5-1 chi
8	545	93.8	239	9 ADV98533	Adv98533 Novel chi
9	545	93.8	661	9 ADV92490	Adv92490 FL/FC/chs
10	545	93.8	661	9 ADV98553	Adv98553 Novel chi
11	544	93.6	112	5 AAE29266	Aae29266 S. aureus
12	544	93.6	112	8 ADU39970	Adu39970 Antibody
13	544	93.6	116	9 AEA38741	Aea38741 Murine an
14	544	93.6	667	9 AEA38768	Aea38768 Humanized
15	543	93.5	112	5 AAE29264	Aae29264 S. aureus
16	543	93.5	113	8 ADO32094	Ado32094 Humanised
17	541	93.1	113	7 ADB97820	Adb97820 HEV relat
18	539	92.8	112	2 AAR54933	Aar54933 MAB 022 V
19	535	92.1	112	5 AAE29268	Aae29268 S. aureus
20	534	91.9	272	5 AEG31024	Abg31024 Synthetic
21	534	91.9	272	7 ADM25453	Adm25453 Binding d
22	534	91.9	272	7 ADM42728	Adm42728 Synthetic
23	534	91.9	272	9 AEB95396	Aeb95396 Mouse G28
24	534	91.9	272	9 AEB94430	Aeb94430 Mouse ant

25	527	90.7	263	2 AAW90236	Aaw90236 Anti-B7.2
26	527	90.7	268	2 AAW90222	Aaw90222 Anti-B7.2
27	527	90.7	268	2 AAW90228	Aaw90228 Anti-B7.1
28	527	90.7	273	2 AAW90224	Aaw90224 Anti-B7.1
29	527	90.7	556	2 AAW90218	Aaw90218 Bispecific
30	527	90.7	580	2 AAW90217	Aaw90217 Bispecific
31	525	90.4	144	9 ADM47080	Adw47080 Light cha
32	522	89.8	132	9 AEB08042	Aeb08042 HLA-DR sp
33	522	89.8	238	8 ADL23052	Adl23052 Mouse/hum
34	522	89.8	238	8 ADS88793	Ads88793 A mouse/h
35	522	89.8	238	9 AEB08041	Aeb08041 Murine/hu
36	520	89.5	113	2 AAR92215	Aar92215 LL2 Mab V
37	520	89.5	113	2 AAW27695	Aaw27695 Variable
38	520	89.5	113	7 ADC97685	Adc97685 Mouse mon
39	520	89.5	244	8 ADG17479	Adg17479 Anti-CD22
40	520	89.5	244	8 ADG17485	Adg17485 Anti-CD22
41	520	89.5	244	8 ADG17476	Adg17476 Anti-CD22
42	520	89.5	244	8 ADG17478	Adg17478 Anti-CD22
43	519	89.3	244	8 ADG17481	Adg17481 Anti-CD22
44	519	89.3	244	8 ADG17486	Adg17486 Anti-CD22
45	517	89.0	244	8 ADG17477	Adg17477 Anti-CD22

ALIGNMENTS

RESULT 1
ADO32092
ID ADO32092 standard; protein; 113 AA.
XX
AC ADO32092;
XX
DT 12-AUG-2004 (first entry)
XX
DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.
XX
KW anti-CD33 antibody; epitope-binding fragment;
KW complementarity-determining region; CDR; immunoconjugate; cytostatic;
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
KW light chain.
XX
OS Mus musculus.
XX
PN WO2004043344-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US032737.
XX
PR 07-NOV-2002; 2002US-0424332P.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Hoffee MG, Tavares D, Lutz RJ;
DR WPI; 2004-411619/38.
DR N-PSDB; ADO32139.
XX
PT New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.
XX
PS Claim 8; SEQ ID NO 8; 124pp; English.
XX
CC The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementary-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoconjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain
 CC variable region, which is used in an example from the present invention.
 XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 581; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.7e-39;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60
 |||||
 DB 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60
 |||||

QY 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYVCHQYLSRRTFGGKLEIKR 113
 |||||
 DB 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYVCHQYLSRRTFGGKLEIKR 113
 |||||

RESULT 2
 AD032146
 ID AD032146 standard; protein; 114 AA.
 XX
 AC AD032146;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.
 XX
 KW anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.
 XX
 OS Mus musculus.
 XX
 PN WO2004043344-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032737.
 XX
 PR 07-NOV-2002; 2002US-0424332P.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX
 DR WPI; 2004-411619/38.
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.
 XX
 PS Example 3; SEQ ID NO 62; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody light chain homologous
 CC amino acid sequence, which is used in an example from the present
 CC invention.
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 581; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.7e-39;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60
 |||||
 DB 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60
 |||||

QY 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYVCHQYLSRRTFGGKLEIKR 113
 |||||
 DB 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYVCHQYLSRRTFGGKLEIKR 113
 |||||

RESULT 3
 ADX37184
 ID ADX37184 standard; protein; 113 AA.
 XX
 AC ADX37184;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Murine SMS-1 antibody, mSMS-1, light chain variable region, SEQ ID 4.
 XX
 KW Cytostatic; Gene Therapy; light chain variable region; SMS-1; neoplasm;
 KW melanoma; breast tumor; hepatocellular carcinoma.
 XX
 OS Mus musculus.
 XX
 PN US2005031617-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 26-NOV-2003; 2003US-00722849.

```

XX 06-JUN-2003; 2003CN-00129123.
PR 25-NOV-2003; 2003CN-01119926.
XX (MAJJ/) MA J.
XX (GUOY/) GUO Y.
XX
PI Ma J, Guo Y;
XX
XX WPI; 2005-131967/14.
DR N-PSDB; ADX37188.
XX
XX New antibody that competitively inhibits the immunospecific binding of a
PT human SMS-1 specific monoclonal antibody to a SMS-1 target antigen,
PT useful for diagnosing or treating neoplasms, e.g. melanoma or breast
PT cancer.
XX
XX Claim 11; SEQ ID NO 4; 40pp; English.
XX
XX The present invention relates to antibodies which are specific for the
CC cancer associated antigen SMS-1. The antibodies are useful for assaying
CC for SMS-1 antigen in a sample, which is useful for the prognosis or
CC diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular
CC carcinoma. The present sequence is a variable region of one such anti-SMS
CC -1 antibody.
XX
XX SQ Sequence 113 AA;
Query Match 93.8%; Score 545; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.3e-36;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTR 60
DB 1 NIMWTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKNYLAWYQKFGSPKLLIYWASTR 60
QY 61 ESGVPRDFTGSGSGTDTLTITISSVQSEDLAIVYCHQYLSRRTFGGKLEIKR 113
DB 61 ESGVPRDFTGSGSGTDTLTITISSVQAEADLAIVYCHQYFSSTYTFGGGKLEIKR 113
RESULT 4
AEA88701
ID AEA88701 standard; protein; 113 AA.
XX
XX AEA88701;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mouse anti-SMS-1 antibody light chain variable region, SEQ ID: 4.
XX
XX cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
KW hepatocellular carcinoma; immunotherapy; light chain variable region;
KW SMS-1.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Key 24..40
FT Region /note= "Variable region"
FT Region 56..62
FT Region /note= "Variable region"
FT Region 95..102
FT Region /note= "Variable region"
XX
XX WO2005053604-A2.
XX
XX 16-JUN-2005.
XX
XX 04-JUN-2004; 2004WO-US017855.
XX
XX 06-JUN-2003; 2003CN-00129123.
PR 25-NOV-2003; 2003CN-01119926.

```

```

PR 26-NOV-2003; 2003US-00722849.
XX 28-NOV-2003; 2003TW-00133571.
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-435284/44.
DR N-PSDB; AEA88705.
XX
XX New antibody competitively inhibiting immunospecific binding of a human
PT SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful in
PT treating malignancies such as melanoma, breast cancer or hepatocellular
PT carcinoma.
XX
XX Claim 11; SEQ ID NO 4; 85pp; English.
XX
XX The present invention relates to an antibody that competitively inhibits
CC the immunospecific binding of a human SMS-1 specific monoclonal antibody
CC (huSMS-1) to a SMS-1 target antigen. The invention is useful in the
CC fields of cancer biology and immunotherapy, in particular for diagnosing
CC and treating malignancies such as melanoma, breast cancer or
CC hepatocellular carcinoma. The present sequence is the mouse anti-SMS-1
CC antibody light chain variable (VL) region.
XX
XX SQ Sequence 113 AA;
Query Match 93.8%; Score 545; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.3e-36;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTR 60
DB 1 NIMWTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKNYLAWYQKFGSPKLLIYWASTR 60
QY 61 ESGVPRDFTGSGSGTDTLTITISSVQSEDLAIVYCHQYLSRRTFGGKLEIKR 113
DB 61 ESGVPRDFTGSGSGTDTLTITISSVQAEADLAIVYCHQYFSSTYTFGGGKLEIKR 113
RESULT 5
ADV92466
ID ADV92466 standard; protein; 133 AA.
XX
XX ADV92466;
XX
XX 10-MAR-2005 (first entry)
XX
XX Mouse SMS-1 (mSMS-1) light chain variable region protein.
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /note= "signal peptide"
FT Region 21..133
FT Protein /note= "Light chain variable region gene (VL)"
FT Protein 21..133
FT Protein /note= "Mature Mouse SMS-1 (mSMS-1) light chain variable
FT region protein"
XX
XX US2004254108-A1.
XX
XX 16-DEC-2004.
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
PR 25-NOV-2003; 2003CN-01119930.

```

```
XX (MAJJ/) MA J.  
PA (GUOY/) GUO Y.  
XX  
XX  
PI Ma J, Guo Y;  
XX  
DR WPI; 2005-030218/03.  
DR N-PSDB; ADV92465.  
XX  
XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
XX  
XX Example 3; SEQ ID NO 10; 158pp; English.  
PS  
XX  
XX The present invention relates to a chimeric protein having a Flt3 ligand  
CC (FL) or its biologically active fragment and a proteinous or peptidyl  
CC tumoricidal agent. The invention is useful for treating malignancy,  
CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
CC vaccine for eliciting an immune response. The invention is also useful in  
CC gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light  
CC chain variable region protein.  
XX  
XX Sequence 133 AA;  
SQ  
Query Match 93.8%; Score 545; DB 9; Length 133;  
Best Local Similarity 92.0%; Pred. No. 1.6e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQOIPGQSPKLLIYWASTR 60  
Db 21 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 80  
QY 61 ESGVPRDRTGSGSGDTFTLTISVQSEDLAIYCHQYLSRRTFGGKLEIKR 113  
Db 81 ESGVPRDRTGSGSGDTFTLTISVQAEADLAVYCHQYFSYTFGGKLEIKR 133  
RESULT 6  
ADV98529  
ID ADV98529 standard; protein; 133 AA.  
XX  
XX  
AC ADV98529;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Novel chimeric protein-related mSM5-1 light chain protein SeqID10.  
XX protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
XX  
XX Mus sp.  
XX  
XX WO2005001048-A2.  
XX  
XX  
XX 06-JAN-2005.  
XX  
XX 04-JUN-2004; 2004WO-US017765.  
XX  
XX 13-JUN-2003; 2003CN-00129290.  
XX 25-NOV-2003; 2003CN-01119930.  
XX 26-NOV-2003; 2003US-00723003.  
XX 28-NOV-2003; 2003TW-00133577.  
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.  
XX  
XX Ma J, Guo Y;  
XX  
XX WPI; 2005-075540/08.  
XX N-PSDB; ADV98528.  
XX  
XX New chimeric protein for preventing or treating neoplastic conditions,  
PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
```

```
PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
PT agent.  
XX  
XX Example 3; SEQ ID NO 10; 147pp; English.  
XX  
XX This invention relates to a novel chimeric protein comprising an Flt3  
CC ligand, or its biological fragment, and a proteinous or peptidyl  
CC tumoricidal agent. The invention may be useful for the production of  
CC compounds with a cytostatic activity or a vaccine. The composition and  
CC methods are useful for preventing or treating neoplastic conditions, such  
CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
CC sequence is that of a protein which is related to the chimeric proteins  
CC of the invention.  
XX  
XX Sequence 133 AA;  
SQ  
Query Match 93.8%; Score 545; DB 9; Length 133;  
Best Local Similarity 92.0%; Pred. No. 1.6e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQOIPGQSPKLLIYWASTR 60  
Db 21 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 80  
QY 61 ESGVPRDRTGSGSGDTFTLTISVQSEDLAIYCHQYLSRRTFGGKLEIKR 113  
Db 81 ESGVPRDRTGSGSGDTFTLTISVQAEADLAVYCHQYFSYTFGGKLEIKR 133  
RESULT 7  
ADV92470  
ID ADV92470 standard; protein; 239 AA.  
XX  
XX  
AC ADV92470;  
XX  
XX 10-MAR-2005 (first entry)  
XX  
XX SM5-1 chimeric antibody (ChSM) light chain protein.  
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
KW breast cancer; hepatocellular carcinoma.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /label= Signal peptide  
FT 21..239  
FT /note= "Mature SM5-1 chimeric antibody (ChSM) light chain  
FT protein"  
FT 21..133  
FT /note= "Light chain variable region gene (VL)"  
FT 134..239  
FT /note= "Human kappa chain constant cDNA (CL)"  
XX  
XX US2004254108-A1.  
XX  
XX 16-DEC-2004.  
XX  
XX 26-NOV-2003; 2003US-00723003.  
XX  
XX 13-JUN-2003; 2003CN-00129290.  
XX 25-NOV-2003; 2003CN-01119930.  
XX  
XX (MAJJ/) MA J.  
PA (GUOY/) GUO Y.  
XX  
XX Ma J, Guo Y;  
XX  
XX WPI; 2005-030218/03.
```

DR N-PSDB; ADV92469.

XX New chimeric protein comprises an Flt3 ligand and a proteinous or peptidyl

PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,

PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.

XX Example 3; SEQ ID NO 14; 158pp; English.

XX The present invention relates to a chimeric protein having a Flt3 ligand

CC (FL) or its biologically active fragment and a proteinous or peptidyl

CC tumoricidal agent. The invention is useful for treating malignancy,

CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a

CC vaccine for eliciting an immune response. The invention is also useful in

CC gene therapy. The present sequence is the SM5-1 chimeric antibody (CHSM)

CC light chain protein.

XX Sequence 239 AA;

SQ

Query Match 93.8%; Score 545; DB 9; Length 239;

Best Local Similarity 92.0%; Pred. No. 2.7e-36;

Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKNYLAWYQOIPQSPKLLIYWASTR 60

DB 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKQSPKLLIYWASTR 80

QY 61 ESGVPRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSRTFGGKLEIKR 113

DB 81 ESGVPRFTGSGGTDTFTLTISVQAEADLAVYCHQYFSSYTFGGKLEIKR 133

RESULT 8

ADV98533

ID ADV98533 standard; protein; 239 AA.

XX

AC ADV98533;

XX

DT 24-MAR-2005 (first entry)

XX

DE Novel chimeric protein-related CHSM light chain protein SeqID14.

XX

KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;

KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.

XX

OS Mus sp.

OS Synthetic.

XX

PN WO2005001048-A2.

XX

PD 06-JAN-2005.

XX

PF 04-JUN-2004; 2004WO-US017765.

XX

PR 13-JUN-2003; 2003CN-00129290.

PR 25-NOV-2003; 2003CN-01119930.

PR 26-NOV-2003; 2003US-00723003.

PR 28-NOV-2003; 2003TW-00133577.

XX

XX (SYMB-) SYMBIGENE ACQUISITION CO INC.

PA

PI Ma J, Guo Y;

PI

XX WPI; 2005-075540/08.

XX

DR N-PSDB; ADV98532.

XX

XX New chimeric protein for preventing or treating neoplastic conditions,

PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an

PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal

PT agent.

XX

XX Example 3; Fig 9; 147pp; English.

PS

XX This invention relates to a novel chimeric protein comprising an Flt3

CC ligand, or its biological fragment, and a proteinous or peptidyl

CC tumoricidal agent. The invention may be useful for the production of

CC compounds with a cytostatic activity or a vaccine. The composition and

CC methods are useful for preventing or treating neoplastic conditions, such

CC as melanoma, breast cancer or hepatocellular carcinoma. The present

CC sequence is that of a protein which is related to the chimeric proteins

CC of the invention. Note: Two sequences were allocated this SeqID number in

CC the specification, the alternative sequence is shown on page 21.

XX

SQ Sequence 239 AA;

Query Match 93.8%; Score 545; DB 9; Length 239;

Best Local Similarity 92.0%; Pred. No. 2.7e-36;

Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKNYLAWYQOIPQSPKLLIYWASTR 60

DB 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKQSPKLLIYWASTR 80

QY 61 ESGVPRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSRTFGGKLEIKR 113

DB 81 ESGVPRFTGSGGTDTFTLTISVQAEADLAVYCHQYFSSYTFGGKLEIKR 133

RESULT 9

ADV92490

ID ADV92490 standard; protein; 661 AA.

XX

AC ADV92490;

XX

DT 10-MAR-2005 (first entry)

XX

DE FL/Pc/chSMPv fusion protein.

XX

KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;

KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;

KW breast cancer; hepatocellular carcinoma.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT Peptide 1..26

FT /label= Signal peptide

FT Protein 27..661

FT /note= "Mature FL/Pc/chSMPv fusion protein"

FT Region 27..182

FT /note= "Flt3 ligand extracellular region (FLEX)"

FT Region 183..197

FT /note= "Hinge region"

FT Region 198..307

FT /note= "CH2 region"

FT Misc-difference 271

FT /note= "Encoded by TGC"

FT Region 308..414

FT /note= "CH3 region"

FT Region 415..533

FT /note= "Heavy chain variable region gene (VH)"

FT Region 534..556

FT /note= "Linker region"

FT Region 557..661

FT /note= "Light chain variable region gene (VL)"

XX

XX US2004254108-A1.

PN

XX 16-DEC-2004.

XX

XX 26-NOV-2003; 2003US-00723003.

XX

XX 13-JUN-2003; 2003CN-00129290.

PR

XX 25-NOV-2003; 2003CN-01119930.

XX

PA (MAJJ/) MA J.
 PA (GUOY/) GUO Y.
 XX
 PI Ma J, Guo Y;
 XX
 DR WPI; 2005-030218/03.
 DR N-PSDB; ADV92489.
 XX
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
 XX
 PS Claim 23; SEQ ID NO 34; 158pp; English.
 XX
 CC The present invention relates to a chimeric protein having a Flt3 ligand
 CC (FL) or its biologically active fragment and a proteinous or peptidyl
 CC tumoricidal agent. The invention is useful for treating malignancy,
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
 CC vaccine for eliciting an immune response. The invention is also useful in
 CC gene therapy. The present sequence is the FL/Fc/chSMFv fusion protein.
 XX
 SQ Sequence 661 AA;
 Query Match 93.8%; Score 545; DB 9; Length 661;
 Best Local Similarity 92.0%; Pred. No. 7.2e-36;
 Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
 Db 549 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 608
 QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAITYCHQYLSRRTFGGTTKLEIKR 113
 Db 609 ESGVDPDRFTGSGGDTFTLTISVQAEADLAIVYCHQYFSSYTFGGTTKLEIKR 661
 RESULT 10
 ADV98553
 ID ADV98553 standard; protein; 661 AA.
 AC ADV98553;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34.
 XX
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO2005001048-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 04-JUN-2004; 2004WO-US017765.
 XX
 PR 13-JUN-2003; 2003CN-00129290.
 PR 25-NOV-2003; 2003CN-01119930.
 PR 26-NOV-2003; 2003US-00723003.
 PR 28-NOV-2003; 2003TW-00133577.
 XX
 XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
 PA
 XX Ma J, Guo Y;
 PI
 XX WPI; 2005-075540/08.
 DR N-PSDB; ADV98552.
 XX
 XX New chimeric protein for preventing or treating neoplastic conditions,
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an

PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
 PT agent.
 XX
 PS Claim 23; SEQ ID NO 34; 147pp; English.
 XX
 CC This invention relates to a novel chimeric protein comprising an Flt3
 CC ligand, or its biological fragment, and a proteinous or peptidyl
 CC tumoricidal agent. The invention may be useful for the production of
 CC compounds with a cytostatic activity or a vaccine. The composition and
 CC methods are useful for preventing or treating neoplastic conditions, such
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present
 CC sequence is that of a protein which is related to the chimeric proteins
 CC of the invention.
 XX
 SQ Sequence 661 AA;
 Query Match 93.8%; Score 545; DB 9; Length 661;
 Best Local Similarity 92.0%; Pred. No. 7.2e-36;
 Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
 Db 549 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 608
 QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAITYCHQYLSRRTFGGTTKLEIKR 113
 Db 609 ESGVDPDRFTGSGGDTFTLTISVQAEADLAIVYCHQYFSSYTFGGTTKLEIKR 661
 RESULT 11
 AAE29266
 ID AAE29266 standard; protein; 112 AA.
 XX
 AC AAE29266;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE S. aureus Clfa specific monoclonal antibody 12-9VLA-1 protein.
 XX
 KW Clumping factor A; Clfa; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 24. .40
 FT /note= "CDR1"
 FT Region 56. .62
 FT /note= "CDR2"
 FT Region 95. .102
 FT /note= "CDR3"
 XX
 PN WO200272600-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 28-JAN-2002; 2002WO-US002296.
 XX
 PR 26-JAN-2001; 2001US-0264072P.
 PR 12-MAR-2001; 2001US-0274611P.
 PR 18-JUN-2001; 2001US-0298413P.
 PR 30-JUL-2001; 2001US-0308116P.
 XX
 XX (INHI-) INHIBITEX INC.
 PA
 XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
 PI
 XX WPI; 2002-759834/82.
 DR N-PSDB; AAD46865.
 XX
 XX New anti- clumping factor A (Clfa) monoclonal antibody, useful for
 PT treating or preventing Staphylococcus aureus infection e.g. wound

PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
 XX a human or animal.

Claim 11; Page 35; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing *S. aureus*
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC of *S. aureus* ClfA protein, *S. aureus* Clf33 protein, or the *S. aureus* N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is *Staphylococcus aureus* ClfA specific monoclonal
 CC antibody 12-9VLA-1 (variable light sequence) protein

XX Sequence 112 AA;

Query Match 93.6%; Score 544; DB 5; Length 112;
 Best Local Similarity 92.9%; Pred. No. 1.6e-36;
 Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQSPKLLIYWASTR 60
 Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKYLAWYQIQSPKLLIYWASTR 60
 Qy 61 ESGVDPDRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112
 Db 61 ESGVDPDRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112

RESULT 12

ADU39970
 ID ADU39970 standard; protein; 112 AA.

AC ADU39970;

XX 27-JAN-2005 (first entry)

XX Antibody TF9 light chain variable region.

XX cytostatic; gene therapy; human tissue factor; antibody engineering;
 KW blood; coagulation; plasma; diagnosing; cancer.

XX Homo sapiens.

XX WO2004094475-A2.

XX 04-NOV-2004.

XX 21-APR-2004; 2004WO-US012206.

XX 22-APR-2003; 2003US-0464363P.

XX 26-JUN-2003; 2003US-0482498P.

XX 05-APR-2004; 2004US-00816938.

XX (EURO-) EUROCELTIQUE SA.

XX (WANG/) WANG B.

XX Wang B;

XX WPI; 2004-795533/78.

XX N-PSDB; ADU39969.

XX New antibodies capable of binding to human tissue factor and do not

XX inhibit tissue factor mediated blood coagulation compared to a normal

XX plasma control, useful for diagnosing, preventing or treating cancer,
 XX such as breast cancer.

XX Disclosure; SEQ ID NO 31; 134pp; English.

XX The invention relates to an isolated antibody capable of binding to human

CC tissue factor (TF), which does not inhibit tissue factor mediated blood
 CC coagulation compared to a normal plasma control and can initiate an Fc-
 CC mediated mechanism. The composition and methods are useful for
 CC diagnosing, preventing or treating cancer, such as non-small cell lung
 CC cancer, breast cancer, colon cancer or prostate cancer. These may also be
 CC used in screening for agents that may treat or prevent cancer. This
 CC sequence corresponds to the light chain variable region of an anti-human
 CC tissue factor antibody.

XX Sequence 112 AA;

Query Match 93.6%; Score 544; DB 8; Length 112;
 Best Local Similarity 92.9%; Pred. No. 1.6e-36;
 Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQSPKLLIYWASTR 60
 Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKYLAWYQIQSPKLLIYWASTR 60
 Qy 61 ESGVDPDRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112
 Db 61 ESGVDPDRFTGSGGTDTFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112

RESULT 13

AEA38741

ID AEA38741 standard; protein; 116 AA.

XX AEA38741;

XX 11-AUG-2005 (first entry)

XX Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.

XX Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;
 KW cancer cell proliferation inhibitor;
 KW transforming growth factor-beta-antagonist; light chain variable region.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 24..40

FT /note= "Complementarity determining region (CDR) - L1"

FT Region 56..62

FT /note= "Complementarity determining region (CDR) - L2"

FT Region 95..102

FT /note= "Complementarity determining region (CDR) - L3"

XX WO2005050200-A2.

XX 02-JUN-2005.

XX 04-NOV-2004; 2004WO-US036651.

XX 13-NOV-2003; 2003US-0520398P.

XX 31-MAR-2004; 2004US-0557951P.

XX (GETH) GENENTECH INC.

XX Filvaroff EH;

XX WPI; 2005-417772/42.

XX Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.

XX Example 2; SEQ ID NO 1; 109pp; English.

XX The present invention relates to the screening of candidate molecules

CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is murine anti-TGF-beta antibody
 CC (2G7) variable light chain (VL) monoclonal antibody protein.
 XX
 SQ Sequence 116 AA;
 Query Match 93.6%; Score 544; DB 9; Length 116;
 Best Local Similarity 92.0%; Pred. No. 1.7e-36;
 Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
 Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
 QY 61 ESGVDPDRFTGSGSGDFTLTITSSVQSEDLAIVYCHQYLSSRTFGGGTKLEIKR 113
 Db 61 ESGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYCHQYLSSDFTFGGGTKLEIKR 113
 RESULT 14
 ID AEA38768 standard; protein; 667 AA.
 XX AEA38768;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Humanized murine anti-TGF-beta antibody protein, chimL.chimH, SEQ: 28.
 XX
 KW Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;
 KW cancer cell proliferation inhibitor;
 KW transforming growth factor-beta-antagonist; humanized antibody;
 KW chimeric antibody.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 220 /label= Unknown
 FT
 XX WO2005050200-A2.
 XX
 PD 02-JUN-2005.
 XX
 XX 04-NOV-2004; 2004WO-US036651.
 XX
 PR 13-NOV-2003; 2003US-0520398P.
 PR 31-MAR-2004; 2004US-0557951P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Filvaroff EH;
 PI
 XX WPI; 2005-417772/42.
 DR
 XX

PT Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 XX growth/bone metastasis.
 PS Example 2; SEQ ID NO 28; 109pp; English.
 XX
 CC The present invention relates to the screening of candidate molecules
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is humanized murine anti-transforming
 CC growth factor-beta (anti-TGF-beta) antibody (also referred as humanized
 CC monoclonal antibody 2G7) chimeric protein.
 XX
 SQ Sequence 667 AA;
 Query Match 93.6%; Score 544; DB 9; Length 667;
 Best Local Similarity 92.0%; Pred. No. 8.7e-36;
 Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
 Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
 QY 61 ESGVDPDRFTGSGSGDFTLTITSSVQSEDLAIVYCHQYLSSRTFGGGTKLEIKR 113
 Db 61 ESGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYCHQYLSSDFTFGGGTKLEIKR 113
 RESULT 15
 ID AEA29264 standard; protein; 112 AA.
 XX AEA29264;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE S. aureus Clfa specific monoclonal antibody 13-2VLA-1 protein.
 XX
 KW Clumping factor A; Clfa; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /note= "CDR1"
 FT Region 56..62
 FT /note= "CDR2"
 FT Region 95..102
 FT /note= "CDR3"
 XX WO200272600-A2.
 XX
 PD 19-SEP-2002.
 XX
 XX 28-JAN-2002; 2002WO-US002296.
 XX
 PR 26-JAN-2001; 2001US-0264072P.
 PR 12-MAR-2001; 2001US-0274611P.
 PR

PR 18-JUN-2001; 2001US-0298413P.
XX 30-JUL-2001; 2001US-0308116P.
XX (INH1-) INHIBITEX INC.
XX
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759834/82.
DR N-PSDB; AAD46863.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
XX Claim 11; Page 34; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein
XX
XX Sequence 112 AA;
SQ

Query Match 93.5%; Score 543; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.9e-36;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAVSAGEKVTMSCKSQSVFSSQKNYLAWYQOIPQSQPKLLIYWASTR 60
Db 1 NIMLTQSPSSLAVSAGEKVTMSCKSQSVFSSQKNYLAWYQOIPQSQPKLLIYWASTR 60
Qy 61 ESGVPRFTGSGSGTDFLTITSSVQSEDLAIYYCHOYLSRTRGGGKLEIK 112
Db 61 ESGVPRFTGSGSGTDFLTITSSVQSEDLAIYYCHOYLSRTRGGGKLEIK 112

Search completed: May 9, 2006, 01:25:28
Job time : 101.749 secs

THIS PAGE BLANK (USPTO)

Query Match	85.7%; Score 498; DB 2; Length 103;	
Best Local Similarity	92.2%; Pred. No. 8.2e-37;	
Matches	95; Conservative 5; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQOIPQSGPKLLIYWASTR 60	
Db	1 NIMWTQSPSSLAVSAGEKVTMSCKSSQSVYSSNQKNYLAWYQOKPQSGPKLLIYWASTR 60	
Qy	61 ESGVPDRFTGSGGCTDFTLTISVQSEDLAIIYYCHQYLSSRTF 103	
Db	61 ESGVPDRFTGSGGCTDFTLTISVQSEDLAIIYYCHQYLSSVTF 103	
RESULT 3		
S41393	Ig kappa chain V region (12.5H VL) - mouse	
C;Species:	Mus musculus (house mouse)	
C;Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001	
C;Accession:	S41393	
R;Margarette, C.; Gilbert, D.; Brard, F.; Tron, F.		
submitted to the EMBL Data Library, January 1994		
A;Description:	Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN	
A;Reference number:	S41393	
A;Accession:	S41393	
A;Status:	preliminary	
A;Molecule type:	mRNA	
A;Residues:	1-112 <MAR>	
A;Cross-references:	UNIPARC:UPI0000176CCB; EMBL:Z29536	
C;Superfamily:	immunoglobulin V region; immunoglobulin homology	
C;Keywords:	heterotetramer; immunoglobulin	
F;16-96/Domain:	immunoglobulin homology <IM>	
Query Match	85.4%; Score 496; DB 2; Length 112;	
Best Local Similarity	83.9%; Pred. No. 1.3e-36;	
Matches	94; Conservative 11; Mismatches 7; Indels 0; Gaps 0;	
Qy	1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQOIPQSGPKLLIYWASTR 60	
Db	1 DIVMSQSPSSLAVSAGEKVTMSCKSSQSLLYSSNQKNYLAWYQOKPQSGPKLLIYWASTR 60	
Qy	61 ESGVPDRFTGSGGCTDFTLTISVQSEDLAIIYYCHQYLSSRTFGGTTKLEIK 112	
Db	61 DSGVPDRFTGSGGCTDFTLTISVQSEDLAIIYYCHQYLSSRTFGGTTKLEIK 112	
RESULT 4		
S43103	Ig kappa chain V-J region (4B1 VL) - mouse (fragment)	
C;Species:	Mus musculus (house mouse)	
C;Date:	06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001	
C;Accession:	S43103	
R;Gilbert, D.; Brard, F.; Margarette, C.; Delpech, A.; Tron, F.		
submitted to the EMBL Data Library, March 1994		
A;Description:	An idiotype D23-bearing polypeptide, murine anti-DNA monoclonal antibody	
A;Reference number:	S42484	
A;Accession:	S43103	
A;Status:	preliminary	
A;Molecule type:	mRNA	
A;Residues:	1-112 <GL>	
C;Cross-references:	UNIPARC:UPI0000116626; EMBL:Z31353; NID:g467574; PIDN:CAA83231.1; PFI	
A;Superfamily:	immunoglobulin V region; immunoglobulin homology	
C;Keywords:	heterotetramer; immunoglobulin	
F;16-96/Domain:	immunoglobulin homology <IM>	
Query Match	84.0%; Score 488; DB 2; Length 112;	
Best Local Similarity	83.9%; Pred. No. 6.7e-36;	
Matches	94; Conservative 10; Mismatches 8; Indels 0; Gaps 0;	
Qy	1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQOIPQSGPKLLIYWASTR 60	
Db	1 DIVMSQSPSSLAVSAGEKVTMSCKSSQSLNLRKNYLAWYQOKPQSGPKLLIYWASTR 60	
Qy	61 ESGVPDRFTGSGGCTDFTLTISVQSEDLAIIYYCHQYLSSRTFGGTTKLEIK 112	

```
RESULT 7
S26040
Ig kappa chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C;Accession: S26040; S78098
R;Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, 1895, 1990
A;Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody
A;Reference number: S09216; MUID:90245589; PMID:2336368
A;Accession: S26040
A;Molecule type: DNA
A;Residues: 1-138 <OKA>
A;Cross-references: UNIPARC:UPI00001769D0; EMBL:X51742
A;Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue
R;Okamoto, M.
submitted to the EMBL Data Library, February 1990
A;Reference number: S78098
A;Accession: S78098
A;Molecule type: DNA
A;Residues: 1-87, 'w', 89-138 <OKW>
A;Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:G52697; PIDN:CAA36032.1; PID
C;Genetics: 22/1
A;Introns: 22/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-138/Product: Ig kappa chain (fragment) #status predicted <WAT>
F;41-121/Domain: immunoglobulin homology <IMM>

Query Match      83.3%; Score 484; DB 2; Length 138;
Best Local Similarity 79.6%; Pred. No. 1.8e-35;
Matches 90; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTR 60
Db 26 DIVMSQSPSSLTSGVGEKVTMCKSSQSLYSNNQKNYLAWYQIQGSPKLLIYWASTR 85
Qy 61 ESGVPDRFTGSGGTDTFLTISVQSEDLAIIYCHQVLSRTFGGKLEIKR 113
Db 86 ESGVPDRFTGSGGTDTFLTISVQAEADLAVYFCQYYSFLTFGAGTKLEIKR 138

RESULT 8
PT0407
Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PT0407
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0407
A;Molecule type: DNA
A;Residues: 1-113 <BEH>
A;Cross-references: UNIPARC:UPI0000176A05
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      82.8%; Score 481; DB 2; Length 113;
Best Local Similarity 82.3%; Pred. No. 2.7e-35;
Matches 93; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTR 60
Db 1 DIVISQSPSSLAVSAGEKVTMSCKSSQSLNRRKNYLAWYQIQGSPKLLIYWASTR 60
Qy 61 ESGVPDRFTGSGGTDTFLTISVQSEDLAIIYCHQVLSRTFGGKLEIKR 113
Db 61 ECGVPDRFTGSGGTDTFLTISVQAEADLAVYCKQSYNLYTFGGGKLEIKR 113

RESULT 9
S09970
Ig kappa chain V-J region (4C8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09970
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09970
A;Molecule type: mRNA
A;Residues: 1-112 <REI>
A;Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:G55406; PIDN:CAA36151.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      82.3%; Score 478; DB 2; Length 112;
Best Local Similarity 79.5%; Pred. No. 5e-35;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTR 60
Db 1 DIVMSQSPSSLTSGVGEKVTMCKSSQSLYSNNQKNYLAWYQIQGSPKLLIYWASTR 60
Qy 61 ESGVPDRFTGSGGTDTFLTISVQSEDLAIIYCHQVLSRTFGGKLEIKR 112
Db 61 ESGVPDRFTGSGGTDTFLTISVQAEADLAVYFCQYYSFLTFGAGTKLEIKR 112

RESULT 10
S26337
Ig light chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26337; S78449
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26337
A;Molecule type: mRNA
A;Residues: 1-101 <STA>
A;Cross-references: UNIPARC:UPI00001769B0; EMBL:X59193
R;Caton, A.J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S78449
A;Accession: S78449
A;Molecule type: mRNA
A;Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A;Cross-references: UNIPARC:UPI0000115F7F; EMBL:X59193; NID:G52323; PIDN:CAA41903.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-88/Domain: immunoglobulin homology <IMM>

Query Match      81.9%; Score 476; DB 2; Length 101;
Best Local Similarity 90.1%; Pred. No. 6.7e-35;
Matches 91; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 9 SSLAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTRESGVDRF 68
Db 1 SSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQIQGSPKLLIYWASTRESGVDRF 60
Qy 69 TGSQSGTDTFLTISVQSEDLAIIYCHQVLSRTFGGKLEIKR 109
Db 61 IGSQSGTDTFLTISVQAEADLAVYCHQVLSRTFGGKLEIKR 101

RESULT 11
PL0265
Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)
```


R;Klobeck, H.G.; Bornkamm, G.W.; Combratio, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A;Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ
A;Reference number: A93589; MUID:86041853; PMID:2997712
A;Accession: A01904
A;Molecule type: DNA
A;Residues: 1-133 <KLO>
A;Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00022; GB:X51570; NID:g33
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV
A;Cross-references: GDB:119341; OMIM:146980
A;Map position: 2p12-2p12
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM>
F;44-60/Region: complementarity-determining 1
F;61-75/Region: framework 2
F;76-82/Region: complementarity-determining 2
F;83-114/Region: framework 3
F;115-122/Region: complementarity-determining 3
F;123-133/Region: framework 4
F;43-114/Disulfide bonds: #status predicted

Query Match 80.7%; Score 469; DB 1; Length 133;
Best Local Similarity 77.0%; Pred. No. 3.6e-34;
Matches 87; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQOIPQSPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSNKNYLAWYQOQPGPPKLLIYWASTR 80

Qy 61 ESGVPDRFTGSGGTDFTLTISSVQSEDLAIYYCHOYLSRTFGGKLEIKR 113
Db 81 ESGVPDRFSGSGGTDFTLTISSLAQEDVAIYYCQYDTIPTFGGKVEIKR 133

Search completed: May 9, 2006, 01:33:51
Job time : 17.1212 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:41 ; Search time 103.461 Seconds
(without alignments)

770.577 Million cell updates/sec

Title: US-10-700-632-8

Perfect score: 591

Sequence: 1 NIMLTQSPSSLAWSAGEKVT.....CHOYLSSRTFGGKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05-80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	80.7	133	1 QV4B_HUMAN	P06313 homo sapien
2	463.5	79.8	240	2 Q52164_MOUSE	Q52164 mus musculu
3	458.5	78.9	114	1 KV4A_HUMAN	P01625 homo sapien
4	451.5	77.7	134	1 KV4C_HUMAN	P06314 homo sapien
5	447.5	77.0	235	2 Q6K805_MOUSE	Q6K805 mus musculu
6	421	72.5	121	1 KV4D_HUMAN	P06312 homo sapien
7	400.5	68.9	109	1 KV4D_HUMAN	P83593 homo sapien
8	384	66.1	109	2 Q9UL78_HUMAN	Q9UL78 homo sapien
9	382	65.7	129	1 KV3L_HUMAN	P18135 homo sapien
10	376.5	64.8	114	1 KV1A_MOUSE	P01632 mus musculu
11	376	64.7	107	2 Q96SA9_HUMAN	Q96SA9 homo sapien
12	374	64.4	109	1 KV3E_HUMAN	P01623 homo sapien
13	373.5	64.3	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
14	372	64.0	109	1 KV3B_HUMAN	P01620 homo sapien
15	371	63.9	129	1 KV3M_HUMAN	P18136 homo sapien
16	370	63.7	109	1 KV3D_HUMAN	P01622 homo sapien
17	370	63.7	235	2 Q6GMV9_HUMAN	Q6GMV9 homo sapien
18	367.5	63.3	136	1 KV5B_MOUSE	P01634 mus musculu
19	367.5	63.3	236	2 Q6P5S8_HUMAN	Q6P5S8 homo sapien
20	367.5	63.3	238	2 Q58BU4_MOUSE	Q58BU4 mus musculu
21	367	63.2	109	2 Q9UL85_HUMAN	Q9UL85 homo sapien
22	366.5	63.1	236	2 Q6P1L8_HUMAN	Q6P1L8 homo sapien
23	365.5	62.9	99	2 Q9JL74_MOUSE	Q9JL74 mus musculu
24	364.5	62.7	149	1 KV5A_MOUSE	P01633 mus musculu
25	363.5	62.6	108	1 KV1M_HUMAN	P01605 homo sapien
26	362.5	62.4	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
27	361	62.1	109	1 KV3G_HUMAN	P04206 homo sapien
28	360.5	62.0	236	2 Q6P1H7_HUMAN	Q6P1H7 homo sapien
29	360	62.0	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
30	360	62.0	129	1 KV3H_HUMAN	P04207 homo sapien
31	359.5	61.9	108	1 KV1V_HUMAN	P04430 homo sapien

32	359.5	61.9	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
33	359	61.8	109	1 KV3F_HUMAN	P01624 homo sapien
34	359	61.8	110	1 KV3P_MOUSE	P01668 mus musculu
35	359	61.8	235	2 Q6GMW0_HUMAN	O6gmw0 homo sapien
36	359	61.8	235	2 Q6RUF2_HUMAN	O6rpj2 homo sapien
37	358.5	61.7	111	1 KV3L_MOUSE	P01664 mus musculu
38	358.5	61.7	111	1 KV3R_MOUSE	P01670 mus musculu
39	358.5	61.7	240	2 Q6PIH6_HUMAN	Q6pih6 homo sapien
40	355.5	61.2	111	2 Q5F217_MOUSE	O5f217 mus musculu
41	355	61.1	109	2 Q9UL86_HUMAN	Q9ul86 homo sapien
42	354.5	61.0	108	1 KV1Y_HUMAN	P80362 homo sapien
43	354.5	61.0	236	2 Q6PITS_HUMAN	Q6pits homo sapien
44	354.5	61.0	238	2 Q6GJS7_MOUSE	O6gj67 mus musculu
45	353	60.8	239	2 Q8NEK0_HUMAN	Q8nek0 homo sapien

ALIGNMENTS

RESULT 1

ID	KV4B_HUMAN	STANDARD;	PRT;	133 AA.
AC	P06313;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig kappa chain V-IV region JI precursor.			
OS	Homo sapiens (Human)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
NCBI_TaxID=9606;				
[1]	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=86041853; PubMed=2997712;			
RX	Zachau H.G.; Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,			
RA	"Subgroup IV of human immunoglobulin K light chains is encoded by a			
RT	single germline gene."			
RL	Nucleic Acids Res. 13:6515-6529 (1985).			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
EMBL; Z00022; CAA77317.1; -; Genomic_DNA.				
DR	PIR; A01904; K4HUJ1.			
DR	HSSP; P01625; ILVE.			
DR	SMR; P06313; 21-133.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 133			
FT	REGION 21 43			
FT	REGION 44 60			
FT	REGION 61 75			
FT	REGION 76 82			
FT	REGION 83 114			
FT	REGION 115 132			
FT	REGION 123 132			
FT	REGION 133 133			
FT	DISULFID 43 114			
FT	NON_TER 133 133			
SQ	SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;			

Query Match

80.7%; Score 469; DB 1; Length 133;

Best Local Similarity 77.2%; Pred. No. 4.4e-41;
Matches 88; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

[illegible]

```

RESULT 3
KV4A_HUMAN          STANDARD;          PRT;    114 AA.
ID   KV4A_HUMAN
AC   P01625;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region Len.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
NCBI_TaxID=9606;
[1]
RN   NCBI_PROTEIN_SEQUENCE.
RP   MEDLINE=76004342; PubMed=50995;
RA   Schneider M., Hilechmann N.;
RT   "The primary structure of a monoclonic immunoglobulin-L-chain of
RL   subgroup IV of the kappa type (Bence-Jones protein Len).";
[2]   Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN   NCBI_SEQUENCE REVISION TO 9.
RA   Salomon A.;
RL   Submitted (AUG-1996) to Swiss-Prot.
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
-----
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.

```

DR	PDB; 2LVE; X-ray; @=1-114.
DR	PDB; 3LVE; X-ray; @=1-114.
DR	PDB; 4LVE; X-ray; A/B=1-114.
DR	PDB; 5LVE; X-ray; A=1-114.
DR	GQ; GO:0005576; C:extracellular region; NAS.
DR	GQ; GO:0003823; F:antigen binding; NAS.
DR	GQ; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; IG; 1.
DR	PROSITE; PS00835; IG LIKE; 1.
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;
KW	Immunoglobulin domain; Immunoglobulin V region.
FT	REGION 1 23 Framework-1.
FT	REGION 24 40 Complementarity-determining-1.
FT	REGION 41 55 Framework-2.
FT	REGION 56 62 Complementarity-determining-2.
FT	REGION 63 94 Framework-3.
FT	REGION 95 101 Complementarity-determining-3.
FT	REGION 102 113 Framework-4.
FT	DISULFID 23 94 By similarity.
FT	NON_TER 114 114
FT	STRAND 4 7

FT	STRAND	4	7

```
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT STRAND 25 31
FT STRAND 30 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 74 75
FT TURN 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 78.9%; Score 458.5; DB 1; Length 114;
Best Local Similarity 76.3%; Pred. No. 6.3e-41;
Matches 87; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKPGQPKLLIYWASTR 60

Qy 61 ESGVPRDFTGSGGTDTLTITSSVQSEDLAIIYCHQYLS--RTFGGQTKLEIKR 113
Db 61 ESGVPRDFTGSGGTDTLTITSSVQSEDVAIIYCHQYLS--RTFGGQTKLEIKR 114

RESULT 4
KV4C HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
[2]
RN SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X02990; CAA26733.1; -; mRNA.
DR HSSP; P01625; ILVE.
DR SMR; P06314; 21-134.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
```

```
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT REGION 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 77.7%; Score 451.5; DB 1; Length 134;
Best Local Similarity 74.6%; Pred. No. 4.2e-40;
Matches 85; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRDFTGSGGTDTLTITSSVQSEDLAIIYCHQYLS--RTFGGQTKLEIKR 113
Db 81 ESGVPRDFTGSGGTDTLTITSSVQSEDVAIIYCHQYLS--RTFGGQTKLEIKR 134

RESULT 5
Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
ID Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SCFV B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments."
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; IKCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 77.0%; Score 447.5; DB 2; Length 255;
Best Local Similarity 79.8%; Pred. No. 2.4e-39;
Matches 91; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 137 DIVMTQSPDSLAVSAGEKVTMSCKSQSVLYSSNKNYLAWYQQKPGQPKLLIYWASTR 196

Qy 61 ESGVPRDFTGSGGTDTLTITSSVQSEDLAIIYCHQYLS--RTFGGQTKLEIKR 112
Db 61 ESGVPRDFTGSGGTDTLTITSSVQSEDVAIIYCHQYLS--RTFGGQTKLEIKR 112
```

```
Db 197 ESGVDPDRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249

RESULT 6
KV40 HUMAN
ID KV40 HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=86041853; PubMed=2997712;
RX Klobbeck H.G., Bornkaum G.W., Combriato G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z00023; CAA77318.1; -; Genomic DNA.
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR SMR; P06312; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Immunoglobulin V region; Signal.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT REGION 21 43 Framework-1.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD418BD33974 CRC64;

Query Match 72.5%; Score 421; DB 1; Length 121;
Best Local Similarity 77.0%; Pred. No. 6.8e-37;
Matches 77; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249
Db 81 ESGVDPDRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249

RESULT 7
KV40 HUMAN
ID KV40 HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC SMR; P83593; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 40 Complementarity-determining-1.
FT REGION 41 55 Framework-2.
FT REGION 56 62 Complementarity-determining-2.
FT REGION 63 94 Framework-3.
FT REGION 95 101 Complementarity-determining-3.
FT REGION 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA1E12A0B CRC64;

Query Match 68.9%; Score 400.5; DB 1; Length 109;
Best Local Similarity 68.8%; Pred. No. 9.3e-35;
Matches 75; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATINCSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249
Db 61 ESGVDPDRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249

RESULT 8
KV40 HUMAN
ID Q9UL78 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```

OC Homo.
 RN NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1373487;
 RA Zebede S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
 RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
 RT "Human combinatorial antibody libraries to hepatitis B surface
 antigen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179 (1992).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 distributed over a large portion of the V kappa locus and do not show
 somatic mutation.";
 RL Eur. J. Immunol. 23:391-397 (1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=155291;
 RA Martin T., Buffy S.F., Carson D.A., Kipps T.J.;
 RT "Evidence for somatic selection of natural autoantibodies.";
 RL J. Exp. Med. 175:983-991 (1992).
 DR EMBL: AF035036; AAD56272.1; -; mRNA.
 DR PIR: A30601; A30601.
 DR PIR: A30601; A30601.
 DR PIR: B30601; B30601.
 DR PIR: B30601; B30601.
 DR PIR: B30601; B30601.
 DR PIR: C30601; C30601.
 DR PIR: C30601; C30601.
 DR PIR: C30601; C30601.
 DR PIR: C30601; C30601.
 DR PIR: D30601; D30601.
 DR PIR: D30601; D30601.
 DR PIR: D30601; D30601.
 DR PIR: D30601; D30601.
 DR PIR: F30601; F30601.
 DR PIR: F30601; F30601.
 DR PIR: F30601; F30601.
 DR PIR: G30601; G30601.
 DR PIR: G30601; G30601.
 DR PIR: H30601; H30601.
 DR PIR: H30601; H30601.
 DR PIR: H4151; H4151.
 DR PIR: I30601; I30601.
 DR PIR: PH0963; PH0963.
 DR PIR: PH0964; PH0964.
 DR PIR: PH0965; PH0965.
 DR PIR: S33988; S33988.
 DR PIR: S34096; S34096.
 DR HSSP: P01625; 1EK3.
 DR SMR: Q9UL78; 1-109.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR NON_TER 109 109
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;
 Query Match 66.1%; Score 384; DB 2; Length 109;
 Best Local Similarity 68.1%; Pred. No. 5.4e-33;
 Matches 77; Conservative 18; Mismatches 12; Indels 6; Gaps 3;
 QY 2 IMLTQSPSSLAIVAGKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
 DB 2 IVLTQSPGTLSPGERATLSCRAQSV--SSS---YLAWYQKPKQAPRLIYGASSRA 56

QY 62 SGVDRFTSGSGTDFLTITSSVQSEDIAIYCHQYLSS-RTFGGKTKLEIKR 113
 DB 57 TGIPDRFSGSGTDFLTITSLRLEPEDCAVYVCCQYGGSSPLTFGGGKTKLEIKR 109
 RESULT 9
 KV3L HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-III region HAH precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852 (1988).
 CC -I- DISEASE: The protein is one of the surface immunoglobulin M
 CC autoantibodies expressed in patients with chronic lymphocytic
 CC leukemia.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR: P18135; 21-129.
 DR HSSP: P01625; 1EEQ.
 DR SMR: P18135; 21-129.
 DR EMBL: ENSG00000169769; Homo sapiens.
 DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 129 Ig kappa chain V-III region HAH.
 FT REGION 21 43 Framework-1.
 FT REGION 44 55 Complementarity-determining-1.
 FT REGION 56 70 Framework-2.
 FT REGION 71 77 Complementarity-determining-2.
 FT REGION 78 109 Framework-3.
 FT REGION 110 118 Complementarity-determining-3.
 FT REGION 119 129 UKI segment.
 FT DISULFID 43 109 By similarity.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C5292772774D0 CRC64;
 Query Match 65.7%; Score 382; DB 1; Length 129;
 Best Local Similarity 67.3%; Pred. No. 1.1e-32;
 Matches 76; Conservative 18; Mismatches 13; Indels 6; Gaps 3;
 QY 2 IMLTQSPSSLAIVAGKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
 DB 22 IVLTQSPGTLSPGERATLSCRAQSV--SSS---YLAWYQKPKQAPRLIYGASSRA 76
 QY 62 SGVDRFTSGSGTDFLTITSSVQSEDIAIYCHQY-LSRTPGGGKTKLEIKR 113
 DB 77 TGIPDRFSGSGTDFLTITSLRLEPEDFAVYVCCQYGGTSPRTFGGKTKLEIKR 129


```

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SSYLNIWYQKPKGKAPKLLIYAASL 54

Qy 61 ESVGVPDRFPGSGSGTDFLTITSSVQSEDLAIYYCHOYLS-SRTFGGKLEIKR 113
Db 55 QSGVPSRFGSGSGTDFLTITSSLPQEDFAVYCCQSYSTLTFGGKVEIKR 107

RESULT 12
KV3B_HUMAN
ID -KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Last Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.;"
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR; A01896; K3HUL.
DR HSP; P01625; ILVE.
DR SMR; P01623; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBBE CRC64;

Query Match 64.4%; Score 374; DB 1; Length 109;
Best Local Similarity 63.7%; Pred. No. 6.3e-32;
Matches 72; Conservative 18; Mismatches 17; Indels 6; Gaps 2;

Qy 2 IMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQQIPGQSPKLLIYWASTRE 61
Db 2 IVLTQSPGTLSPGERATLSCRASQSV-----SSGYLGWYQKPKGQAPRLIIYGASSRA 56

Qy 62 SGVPDRFPGSGSGTDFLTITSSVQSEDLAIYYCHOYLS-SRTFGGKLEIKR 113
Db 57 TGIPDRFPGSGSGTDFLTITSLRPEDFAVYCCQYGLRGTFGGKVEIKR 109

RESULT 13
Q9UL70_HUMAN
ID Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.;"
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.;"
RL J. Exp. Med. 174:1639-1652(1991).
DR EMBL; AF035044; AAD56280.1; -; mRNA.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBMW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 64.3%; Score 373.5; DB 2; Length 108;
Best Local Similarity 64.9%; Pred. No. 7e-32;
Matches 74; Conservative 17; Mismatches 16; Indels 7; Gaps 2;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SNLYAWYQKPKGKPKSLIYAASL 54

Qy 61 ESVGVPDRFPGSGSGTDFLTITSSVQSEDLAIYYCHOYLS-SRTFGGKLEIKR 113
Db 55 QSGVPSRFGSGSGTDFLTITSSLPQEDFAVYCCQYNSAPRTFGGKLEIKR 108

RESULT 14
KV3B_HUMAN
ID -KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Last Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.;"
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.

```

```

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01892; K3HUHI.
CC HSSP; P01625; LLVE.
CC SMR; P01620; 1-109.
CC DR GO; GO:0005576; C:extracellular region; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin domain; Immunoglobulin V region; Signal.
CC FT CHAIN 1 20
CC FT REGION 21 129
CC FT REGION 21 43
CC FT REGION 44 55
CC FT REGION 56 70
CC FT REGION 71 77
CC FT REGION 78 109
CC FT REGION 110 118
CC FT REGION 119 129
CC FT DISULFID 43 109
CC FT NON_TER 129 129
CC SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646PFB4 CRC64;
CC
CC Query Match 64.0%; Score 372; DB 1; Length 109;
CC Best Local Similarity 62.8%; Pred. No. 1e-31;
CC Matches 71; Conservative 22; Mismatches 14; Indels 6; Gaps 2;
CC
CC QY 2 IMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE 61
CC Db 2 IVLTQSPGTLISLSPGERATLSCRASQSV-----SNSYLAWYQQKPKQAPRLLIYGASSRA 56
CC
CC QY 62 SGVPRDPTGSGSGTDFTLTITISVQSEDLAIYYCHQYLSS-RTFGGKTLEIKR 113
CC Db 57 TGIPDRFSGSGSGTDFTLTISRLEPDDFAVYCCQYGSQPQTFGGSKVEIKR 109
CC
CC RESULT 15
CC KV3M_HUMAN STANDARD; PRT; 129 AA.
CC AC P18136;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
CC DE Ig kappa chain V-II region HIC precursor.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
CC OC Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE.
CC RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
CC RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
CC RT "Autoantibody-associated kappa light chain variable region gene
CC RT expressed in chronic lymphocytic leukemia with little or no somatic
CC RT mutation. Implications for etiology and immunotherapy.";
CC RL J. Exp. Med. 167:840-852(1988).
CC CC -! DISEASE: The protein is one of the surface immunoglobulin M
CC CC autoantibodies expressed in patients with chronic lymphocytic
CC CC leukemia.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; P10021; K3HUHI.
CC HSSP; P01625; 1EEQ.
CC SMR; P18136; 21-129.
CC DR Ensembl; ENSG00000169769; Homo sapiens.
CC DR GO; GO:0005576; C:extracellular region; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.

```

```

DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT REGION 21 43
FT REGION 44 55
FT REGION 56 70
FT REGION 71 77
FT REGION 78 109
FT REGION 110 118
FT REGION 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;
CC
CC Query Match 63.9%; Score 371; DB 1; Length 129;
CC Best Local Similarity 66.4%; Pred. No. 1.6e-31;
CC Matches 75; Conservative 18; Mismatches 14; Indels 6; Gaps 3;
CC
CC QY 2 IMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE 61
CC Db 22 IVLTQSPGTLISLSPGERATLSCRASQSV-----YLAWYQQKPKQAPRLLIYGASSRA 76
CC
CC QY 62 SGVPRDPTGSGSGTDFTLTITISVQSEDLAIYYCHQYLSS-RTFGGKTLEIKR 113
CC Db 77 TGIPDRFSGSGSGTDFTLTISRLEPDDFAVYCCQYGSQPQTFGGKTVEIKR 129
CC
CC Search completed: May 9, 2006, 01:32:36
CC Job time : 103.461 secs

```


GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 25.4372 Seconds
(without alignments)
367.271 Million cell updates/sec

Title: US-10-700-632-8

Perfect score: 581

Sequence: 1 NIMLTQSPSSLAWSAGEKVT.....CHOYLSRRTFGGKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	92.8	112	2	US-08-435-516-28
2	520	89.5	113	1	US-08-690-102A-2
3	520	89.5	113	2	US-09-127-902-2
4	520	89.5	113	2	US-09-155-107-2
5	520	89.5	113	4	PCT-US95-09641-2
6	505	86.9	110	2	US-10-146-305-7
7	503	86.6	112	1	US-07-916-098A-15
8	498.5	85.8	113	4	PCT-US93-08435-4
9	498	85.7	259	2	US-09-419-788-115
10	488	84.0	114	2	US-08-929-856-66
11	488	84.0	219	1	US-08-353-400-34
12	488	84.0	229	1	US-08-353-400-37
13	487	83.8	288	2	US-09-423-439-38
14	487	83.8	673	2	US-09-423-439-32
15	485.5	83.6	114	1	US-08-428-257A-76
16	485.5	83.6	114	2	US-07-987-264-16
17	483	83.1	113	1	US-08-690-102A-6
18	483	83.1	113	2	US-09-127-902-6
19	483	83.1	113	2	US-09-155-107-6
20	483	83.1	113	4	PCT-US95-09641-6
21	482.5	83.0	220	2	US-08-952-235-1
22	482.5	83.0	220	2	US-09-669-971-1
23	482	83.0	249	2	US-09-297-181-4
24	481.5	82.9	113	2	US-08-483-749A-16
25	480	82.6	109	1	US-08-308-494A-23
26	478	82.3	132	2	US-09-627-896B-4
27	478	82.3	132	2	US-09-339-596A-4

28	475	81.8	114	2	US-08-929-856-189	Sequence 189, App
29	474.5	81.7	113	4	PCT-US93-08435-6	Sequence 6, Appli
30	470	80.8	265	1	US-08-403-853-16	Sequence 16, Appl
31	469.5	80.8	113	4	PCT-US93-08435-8	Sequence 8, Appli
32	469	80.7	110	2	US-08-957-001B-5	Sequence 5, Appli
33	469	80.7	110	2	US-08-957-001B-24	Sequence 24, Appl
34	469	80.7	110	2	US-09-496-301-5	Sequence 5, Appli
35	469	80.7	110	2	US-09-496-301-24	Sequence 24, Appl
36	469	80.7	241	1	US-07-916-098A-56	Sequence 56, Appl
37	468.5	80.6	114	2	US-09-232-290-12	Sequence 12, Appl
38	468.5	80.6	456	2	US-09-495-880A-11	Sequence 11, Appl
39	468	80.6	112	2	US-08-435-516-4	Sequence 4, Appli
40	468	80.6	113	2	US-09-823-746-2	Sequence 2, Appli
41	468	80.6	301	1	US-08-661-052-14	Sequence 14, Appl
42	468	80.6	301	2	US-09-188-082-14	Sequence 14, Appl
43	468	80.6	301	2	US-09-364-088-14	Sequence 14, Appl
44	468	80.6	301	2	US-09-102-716-14	Sequence 14, Appl
45	468	80.6	352	2	US-09-203-958A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-435-516-28

; Sequence 28, Application US/08435516

; Patent No. 6500931

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR

; NUMBER OF INVENTIONS: 28

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,516

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384

; FILING DATE: 04-NOV-1992; -02-NOV-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-013

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; US-08-435-516-28

Query Match 92.8%; Score 539; DB 2; Length 112;

Best Local Similarity 92.0%; Pred. No. 1.7e-46;

Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAWSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 NIWMTQSPSSLAWSAGEKVTMSCKSQSVLYSSNQKNYLAWYQQKPGSPKLLIYWASTR 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ESGVPRFRFGSGSGTDFTLTISSVQSEDIAIYCHQYLSRRTFGGKLEIK 112

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ESGVPRFRFGSGSGTDFTLTISSVQAEADLAVYCHQYLSRRTFGGKLEIK 112

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```
RESULT 2
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-690-102A-2

Query Match 89.5%; Score 520; DB 1; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGDTFTLTISRQVDEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA

Query Match 89.5%; Score 520; DB 2; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGDTFTLTISRQVDEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-155-107-2

Query Match 89.5%; Score 520; DB 2; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGDTFTLTISRQVDEDLAIYYCHQYLSSRTFGGKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRRTGGGKLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTGGGKLEIKR 113

RESULT 5

PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 89.5%; Score 520; DB 4; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRRTGGGKLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTGGGKLEIKR 113

RESULT 6

US-10-146-305-7
; Sequence 7, Application US/10146305
; Patent No. 6939956
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI7440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-7

Query Match 86.9%; Score 505; DB 2; Length 130;
Best Local Similarity 84.1%; Pred. No. 5.1e-43;
Matches 95; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRRTGGGKLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTGGGKLEIKR 113

RESULT 7

US-07-916-098A-15
; Sequence 15, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-15

Query Match 86.6%; Score 503; DB 1; Length 112;
Best Local Similarity 84.8%; Pred. No. 6.8e-43;
Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSAHKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRRTGGGKLEIKR 112
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTGGGKLEIKR 112

```
RESULT 8
PCT-US93-08435-4
; Sequence 4, Application PC/TU9308435
; GENERAL INFORMATION:
; APPLICANT: Smithline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-4

Query Match 85.8%; Score 498.5; DB 4; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.9e-42;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DQLTQSPSLAVSVGKVTMSCKSSQLLYSSNQKNYLAWYQQKQSPKLLIYWASTR 60

QY 61 ESGVPRDFTGSGGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGTTKLEIK 112
Db 61 ESGVPRDFTGRSGTGDTFLTITSSVKAEDLAVYYCQYYSYVPTFGGTTKLEIK 113

RESULT 9
US-09-419-788-115
; Sequence 115, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
```

```
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; EARLIER FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-115

Query Match 85.7%; Score 498; DB 2; Length 259;
Best Local Similarity 84.1%; Pred. No. 5.6e-42;
Matches 95; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 141 DIVLSQSPSSLAIVSVGKVTMSCKSSQLLYSSNQKNYLAWYQQKQSPKLLIYWASTR 200

QY 61 ESGVPRDFTGSGGTDFTLTITSSVQSEDLAIYYCHQYLSRTFGGTTKLEIKR 113
Db 201 ESGVPRDFTGSGGTDFTLTITNSVKAEDLAVYYCQYYSYVTFGAGTKLEIKR 253

RESULT 10
US-08-929-856-66
; Sequence 66, Application US/08929856
; Patent No. 6136568
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Rose, Floyd
; TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
; TITLE OF INVENTION: ROLLING TEMPLATES
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: ROSE 3.0-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
US-08-929-856-66

Query Match      84.0%; Score 488; DB 2; Length 114;
Best Local Similarity 83.2%; Pred. No. 2.2e-41;
Matches 94; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMSQSPSSLAVSAGEKVTMCKSSQSLNSTRKNFLAWYQQKPGQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ESGVPRFTGSGGTDTFTLTSSVQSEDLAIIYCHQVLSRRTGGGTKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPRFTGSGGTDTFTLTSSVQAEADLAIIYCKQSYTLRTFGGTKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-34

Query Match      84.0%; Score 488; DB 1; Length 219;
Best Local Similarity 84.1%; Pred. No. 4.6e-41;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMSQSPSSLAVSAGEKVTMCKSSQSLNSTRKNFLAWYQQKPGQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ESGVPRFTGSGGTDTFTLTSSVQSEDLAIIYCHQVLSRRTGGGTKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 TSGVPRFTGSGGTDTFTLTSSVQAEADLAIIYCKQSYTLRTFGGTKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-37

Query Match      84.0%; Score 488; DB 1; Length 239;
Best Local Similarity 84.1%; Pred. No. 5.1e-41;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIVMSQSPSSLAVSAGEKVTMCKSSQSLNSTRKNFLAWYQQKPGQSPKLLIYWASTR 80
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ESGVPRFTGSGGTDTFTLTSSVQSEDLAIIYCHQVLSRRTGGGTKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 TSGVPRFTGSGGTDTFTLTSSVQAEADLAIIYCKQSYTLRTFGGTKLEIKR 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38
```

```

/ TITLE OF INVENTION: Compounds to target cells
/
/ NUMBER OF SEQUENCES: 80
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Jules E. Goldberg
/
/ STREET: 261 Madison Avenue
/
/ CITY: New York
/
/ STATE: NY
/
/ COUNTRY: USA
/
/ ZIP: 10016-2391
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/428.257A
/

```

```

// ***** Software Patent Release #1.0, Version #1.25 (EPO) *****
//
// CURRENT APPLICATION DATA:
//   APPLICATION NUMBER:    US/08/428,257A
//   FILING DATE:          07/05/95
//   CLASSIFICATION:        514
//
// INFORMATION FOR SEQ ID NO: 76:
//   SEQUENCE CHARACTERISTICS:
//     LENGTH: 114 amino acids
//     TYPE: amino acid
//     TOPOLOGY: linear
//
// MOLECULE TYPE: protein
// US-08-428-257A-76

```

Query Match	83.6%;	Score 485.5;	DB 1;	Length 114;
Best Local Similarity	82.5%;	Pred.No. 3.8e-41;		
Matches	94;	Conservative 10;	Mismatches 9;	Indels 1; Gaps 1;
Qy	1	NIMLTGSPSLAVSAGEKVTMCKSGSQSVFFSSQNRYLAWYQQIIFGQSPKLLIYYASTR	60	
	:	:::::	:	
Db	1	DVMSGPSLAVSAGVKETMCKSKQSLSLYNKNKIYLAWYQKEQGQSPKLLIYYASTR	60	
	:	:	:	
Qy	61	ESGVPRFTGSGSGDTFLTITISSVQSEDIAIYYCHQYLS-SRTFGGQTKLEIKR	113	
	:	:	:	
Db	61	ESGVPRFTGGGSGDTFLTITISVKAEDLAIVYCOOYVRPRTFGGTGLEIKR	114	
	:	:	:	

Search completed: May 9, 2006, 01:35:41
Job time : 26.4372 secs

Query Match	83.8%	Score 487;	DB 2;	Length 673;
Best Local Similarity	85.0%	Pred. NO. 2.1e-40;		
Matches	96;	Conservative 7;	Mismatches 10;	Indels 0; Gaps 0
Qy	1	NIMLTQSPSSLAVSAGEKVTMTCKSSQSVFTSSQKNYLAWYQIQPGSPKLLIYWASTR	60	
	:	:	:	:
Db	156	DIELSQSPSSLAVSAGEKVTMTCKSSQSLNSTRKKNYLAWYQQRPGSPKLLIYWASTR	215	
	:	:	:	:
Qy	61	ESGVDPDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSRSTFGGCTKLEIKR	113	
	:	:	:	:
Db	216	TSGVDPDRFTGSGSGTDFLTITSSVOAEDLAIIYCHYLSRSTFGGCTKLEIKR	268	
	:	:	:	:

RESULT 15
US-08-428-257A-76
; Sequence 76, Application US/08428257A
; Patent No. 5985808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
;


```
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62

Query Match      100.0%; Score 581; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-10-722-849-4
; Sequence 4, Application US/10722849
; Publication No. US20050031617A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; TITLE OF INVENTION: ASSOCIATED ANTIGEN SMS-1 AND USES THEREOF
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/10/722,849
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-722-849-4

Query Match      93.8%; Score 545; DB 5; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.9e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-11-004-659-4
; Sequence 4, Application US/11004659
; Publication No. US20050232926A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; TITLE OF INVENTION: ASSOCIATED ANTIGEN SMS-1 AND USES THEREOF
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/11/004,659
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/722,849
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113

; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-004-659-4

Query Match      93.8%; Score 545; DB 5; Length 133;
Best Local Similarity 92.0%; Pred. No. 3.4e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQIPGSPKLLIYWASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-10-723-003-10
; Sequence 10, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-10

Query Match      93.8%; Score 545; DB 5; Length 133;
Best Local Similarity 92.0%; Pred. No. 3.4e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQIPGSPKLLIYWASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIYYCHQYLSRRTFGGTTKLEIKR 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-11-004-639-10
; Sequence 10, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
```



```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-10

Query Match          93.8%; Score 545; DB 6; Length 133;
Best Local Similarity 92.0%; Pred. No. 3.4e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOI PQSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPQSPKLLIYWASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIYYCHQVLSRTFGGKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVYYCHQVFSSTFGGKLEIKR 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-10-723-003-14
; Sequence 14, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14

Query Match          93.8%; Score 545; DB 5; Length 239;
Best Local Similarity 92.0%; Pred. No. 6.2e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOI PQSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPQSPKLLIYWASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIYYCHQVLSRTFGGKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVYYCHQVFSSTFGGKLEIKR 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
```

```
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14

Query Match          93.8%; Score 545; DB 6; Length 239;
Best Local Similarity 92.0%; Pred. No. 6.2e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOI PQSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPQSPKLLIYWASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIYYCHQVLSRTFGGKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVYYCHQVFSSTFGGKLEIKR 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-10-723-003-34
; Sequence 34, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-34

Query Match          93.8%; Score 545; DB 5; Length 661;
Best Local Similarity 92.0%; Pred. No. 1.7e-40;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOI PQSPKLLIYWASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 549 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPQSPKLLIYWASTR 608
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIYYCHQVLSRTFGGKLEIKR 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 609 ESGVPRFTGSGSGTDFTLTISVQAEADLAVYYCHQVFSSTFGGKLEIKR 661
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-11-004-639-34
; Sequence 34, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
```

```
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-34

Query Match          93.8%; Score 545; DB 6; Length 661;
Best Local Similarity 92.0%; Pred. No. 1.7e-40;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 549 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 608

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGGTKLEIKR 113
Db 609 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVYCHQYLSRRTFGGGTKLEIKR 661
```

```
RESULT 11
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match          93.6%; Score 544; DB 4; Length 112;
Best Local Similarity 92.9%; Pred. No. 3.6e-41;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGGTKLEIK 112
```

```
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVYCHQYLSRRTFGGGTKLEIK 112

RESULT 12
US-10-816-938-31
; Sequence 31, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-31

Query Match          93.6%; Score 544; DB 5; Length 112;
Best Local Similarity 92.9%; Pred. No. 3.6e-41;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGGTKLEIK 112
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVYCHQYLSRRTFGGGTKLEIK 112
```

```
RESULT 13
US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match          93.5%; Score 543; DB 4; Length 112;
Best Local Similarity 92.0%; Pred. No. 4.4e-41;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60
```


THIS PAGE BLANK (USPTO)

5
4
3
2
1

```

US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P206981
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29

Query Match          93.6%; Score 544; DB 9; Length 666;
Best Local Similarity 92.0%; Pred. No. 1e-32;
Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1  NIMLTQSPSSSLAVSAGEKVTWCKSSQSVFFSSQKNYLAWYQOI PQSQPKLIYWASTR 60
Db      1  DIMWTQSPSSSLAVSAGEKVTWCKSSQSVLYSSNQKNYLAWYQOKPQSQPKLIYWASTR 60

Qy      61  ESGVPRDFTGSGGTDFTLTISVVQSEDLAIYYCHQVLSRRTGGGTKLEIKR 113
Db      61  ESGVPRDFTGSGGTDFTLTISVVQSEDLAVYYCHQVLSRDTGGGTKLEIKR 113

```

```

RESULT 5
US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: PI954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
;
US-11-096-046-29

Query Match      93.6%; Score 544; DB 11; Length 667;
Best Local Similarity 92.0%; Pred. No. 1e-32;
Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NIMLTQSPSSLAIVSAGEKVTWCKSSQSVFSSSSKQNYLAWYQOI PGQSPKLLIYWASTR 60
      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 DIMMTQSPSSLAIVSAGEKVTWCKSSQSVLYSSNQKYLAWYQOKPGQSPKLLIYWASTR 60

```

QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRTPGGGKLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRTPGGGKLEIKR 113

RESULT 6

US-11-136-559-6
; Sequence 6, Application US/11136559
; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 6

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-11-136-559-6

Query Match 93.5%; Score 543; DB 11; Length 112;
Best Local Similarity 92.0%; Pred. No. 3e-33;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRTPGGGKLEIK 112

Db 61 ESGVDRFTGSGGTDFTLTINSVQAEADLAIIYCHQVLSRTPGGGKLEIK 112

RESULT 7

US-11-136-559-14

; Sequence 14, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-11-136-559-14

Query Match 92.1%; Score 535; DB 11; Length 112;

Best Local Similarity 91.1%; Pred. No. 1.1e-32;

Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRTPGGGKLEIK 112

Db 61 ESGVDRFTGSGGTDFTLTISVQAEADLAIIYCHQVLSRTPGGGKLEIK 112

RESULT 8

US-11-136-559-22

; Sequence 22, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 22

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-11-136-559-22

Query Match 91.4%; Score 531; DB 11; Length 112;

Best Local Similarity 91.1%; Pred. No. 2.2e-32;

Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGGTDFTLTISVQSEDLAIIYCHQVLSRTPGGGKLEIK 112

Db 61 ESGVDRFTGSGGTDFTLTISVQAEADLAIIYCHQVLSRTPGGGKLEIK 112

RESULT 9

US-11-136-559-18

; Sequence 18, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea

```
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: FATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; TYPE: PRT
; LENGTH: 112
; ORGANISM: Staphylococcus aureus
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-11-136-559-18

Query Match      88.8%; Score 516; DB 11; Length 112;
Best Local Similarity 86.6%; Pred. No. 2.7e-31;
Matches 97; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 60
DB 1 DIVLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 60

QY 61 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 112
DB 61 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 112

RESULT 10
US-10-512-184-31
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match      84.6%; Score 491.5; DB 9; Length 259;
Best Local Similarity 84.2%; Pred. No. 3.1e-29;
Matches 96; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 60
DB 138 DIVLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 197

QY 61 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 113
```

```
DB 198 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 251

RESULT 11
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match      84.6%; Score 491.5; DB 9; Length 329;
Best Local Similarity 84.2%; Pred. No. 3.8e-29;
Matches 96; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 60
DB 208 DIVLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 267

QY 61 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 113
DB 268 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 321

RESULT 12
US-10-512-184-33
; Sequence 33, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-33

Query Match      82.5%; Score 479.5; DB 9; Length 259;
Best Local Similarity 82.5%; Pred. No. 2.3e-28;
Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 60
DB 138 DIVLTQSPSSSLAVSAGEKVTMSCKSSQSFVFFSSQKQYLAWYQQIPGQSPKLLIYWASTR 197

QY 61 ESGVPRFRFGSGSGTDFTLTITSSVQSEDLAIYYCHQYLS-SRTFGGKLEIKR 113
```


Db 198 ESGVDRFTGSGGDTFTLTISVKAEDLAVYYCQYYSYPTFTFGSGTKLEIKR 251

RESULT 13

US-10-512-184-70

; Sequence 70, Application US/10512184

; Publication No. US20050244901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

; TITLE OF INVENTION: resistance against fungi

; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 70

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: precursor

; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.

US-10-512-184-70

Query Match 82.5%; Score 479.5; DB 9; Length 329;

Best Local Similarity 82.5%; Pred. No. 2.8e-28;

Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60

Db 208 DIVLSQSPSSSLAVLGEKVTMSCKSQSLIYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 267

QY 61 ESGVDRFTGSGGDTFTLTISVQSEDLAIVYCHOYLS-SRTFGGTKLEIKR 113

Db 268 ESGVDRFTGSGGDTFTLTISVKAEDLAVYYCQYYSYPTFTFGSGTKLEIKR 321

RESULT 14

US-11-219-563-71

; Sequence 71, Application US/11219563

; Publication No. US20060088539A1

; GENERAL INFORMATION:

; APPLICANT: Bander, Neil

; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC

; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

; FILE REFERENCE: 13651.001 (BZL-001)

; CURRENT APPLICATION NUMBER: US/11/219,563

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: PCT/US04/06586

; PRIOR FILING DATE: 2004-03-03

; PRIOR APPLICATION NUMBER: US 10/379,838

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: 10/449,379

; PRIOR FILING DATE: 2003-05-30

; NUMBER OF SEQ ID NOS: 144

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 71

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-219-563-71

Query Match 81.7%; Score 474.5; DB 10; Length 113;

Best Local Similarity 82.3%; Pred. No. 2.8e-28;

Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60

Db 1 DIVMTQSPSSSLAVSAGEKVTMSCKSQSLNSGNQKNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGGDTFTLTISVQSEDLAIVYCYHOYLSRRTFGGTKLEIK 112

Db 61 ESGVDRFTGSGGDTFTLTISVQAEADLAVYYCQNDYSYPLTFTFGAGTKLELK 113

RESULT 15

US-11-219-563-91

; Sequence 91, Application US/11219563

; Publication No. US20060088539A1

; GENERAL INFORMATION:

; APPLICANT: Bander, Neil

; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC

; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF

; FILE REFERENCE: 13651.001 (BZL-001)

; CURRENT APPLICATION NUMBER: US/11/219,563

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: PCT/US04/06586

; PRIOR FILING DATE: 2004-03-03

; PRIOR APPLICATION NUMBER: US 10/379,838

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: 10/449,379

; PRIOR FILING DATE: 2003-05-30

; NUMBER OF SEQ ID NOS: 144

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 91

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-219-563-91

Query Match 81.7%; Score 474.5; DB 10; Length 113;

Best Local Similarity 82.3%; Pred. No. 2.8e-28;

Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60

Db 1 DIVMTQSPSSSLAVSAGEKVTMSCKSQSLNSGNQKNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGGDTFTLTISVQSEDLAIVYCYHOYLSRRTFGGTKLEIK 112

Db 61 ESGVDRFTGSGGDTFTLTISVQAEADLAVYYCQNDYSYPLTFTFGAGTKLELK 113

Search completed: May 9, 2006, 02:05:58

Job time : 13.4524 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 106.251 Seconds

(without alignments)
487.964 Million cell updates/sec

Title: US-10-700-632-9

Perfect score: 623

Sequence: 1 QVQLQQPGAEVVRKPGASVRK.....EVLRLYFDVWGQTTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	100.0	118	8	ADO32093 Humanised
2	613	98.4	118	8	ADO32091 Mouse ant
3	609	97.8	117	8	ADO32157 Mouse ant
4	538.5	86.4	121	7	ADJ94605 Chimeric
5	538.5	86.4	121	7	ADJ94607 Chimeric
6	533.5	85.6	120	6	ADJ94601 Mouse ant
7	529	84.9	123	6	Aao27201 Murine an
8	525.5	84.3	140	2	AAR55215 Murine va
9	525.5	84.3	412	4	AAB30694 A fusion
10	525.5	84.3	412	6	ABJ39009 B9E9 scFv
11	524.5	84.2	140	6	ABR55873 Mature r
12	524.5	84.2	140	6	ABU08394 Murine an
13	524.5	84.2	140	7	ADC66270 Mouse ant
14	524.5	84.2	140	7	ADC85690 Murine im
15	524.5	84.2	140	7	ADP73084 Murine FU
16	524.5	84.2	140	7	ADF60661 Protein r
17	524.5	84.2	140	8	ADN49734 Mature va
18	524.5	84.2	140	8	ADU74410 Mouse ant
19	524.5	84.2	140	9	ADV92492 2B8 heavy
20	524.5	84.2	140	9	ADV98555 Novel chi
21	524.5	84.2	140	9	ADZ59909 Glycoprot
22	524.5	84.2	360	5	Aae27924 Human CH2
23	524.5	84.2	360	6	ABB82833 Antibody
24	524.5	84.2	368	9	ADW77074 Heavy cha

25	524.5	84.2	451	8	ADL92472	Adl92472 Antibody
26	524.5	84.2	451	8	ADL92473	Adl92473 Improved
27	524.5	84.2	451	8	ADU68155	Adu68155 Novel var
28	524.5	84.2	451	8	ADU68154	Novel var
29	524.5	84.2	470	3	AAB08026	Aab08026 A dimeric
30	524.5	84.2	470	5	AAE27923	Aae27923 Human C2B
31	524.5	84.2	470	6	ABB82832	Abb82832 Antibody
32	524.5	84.2	470	9	ADV92496	Adv92496 Anti-CD20
33	524.5	84.2	470	9	ADV98559	Adv98559 Novel chi
34	524.5	84.2	626	9	ADV92500	Adv92500 CD20VH/FC
35	524.5	84.2	626	9	ADV98563	Novel chi
36	524.5	84.2	641	9	ADV92502	CD20VH/FC
37	524.5	84.2	641	9	ADV98565	Novel chi
38	524.5	84.2	657	9	ADV92504	FL/FC/CD2
39	524.5	84.2	657	9	ADV98567	Novel chi
40	523	83.9	122	9	ADV21492	Human ant
41	523	83.9	122	9	ADZ83548	CD20 VH.
42	523	83.9	490	9	ADV21539	Mature fo
43	523	83.9	491	9	ADZ83606	CD3 speci
44	523	83.9	491	9	ADZ83598	CD3 speci
45	523	83.9	491	9	ADZ83602	CD3 speci

ALIGNMENTS

RESULT 1

ADO32093
ID ADO32093 standard; protein; 118 AA.

XX
AC ADO32093;

XX
DT 12-AUG-2004 (first entry)

XX
DE Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.

XX
KW anti-CD33 antibody; epitope-binding fragment;

XX
KW complementarity-determining region; CDR; immunoconjugate; cytostatic;

XX
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

XX
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;

XX
KW My9-6; heavy chain.

XX
OS Mus musculus.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
PN WO2004043344-A2.

XX
PD 27-MAY-2004.

XX
PF 05-NOV-2003; 2003WO-US032737.

XX
PR 07-NOV-2002; 2002US-0424332P.

XX
PA (IMMU-) IMMUNOGEN INC.

XX
PI Hoffee MG, Tavares D, Lutz RJ;

XX
DR WPI; 2004-411619/38.

XX
PT New antibodies that bind to CD33, useful for treating a disease

XX
PT associated with CD33 expression, such as myelodysplastic syndrome, acute

XX
PT or chronic myeloid leukaemia.

XX
PS Claim 11; SEQ ID NO 9; 124pp; English.

XX
The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or

CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy
 CC chain variable region, which is used in an example from the present
 CC invention.

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 623; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQGLEWVGVIYPGNDISY 60
 DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQGLEWVGVIYPGNDISY 60
 QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTTVSS 118
 DB 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTTVSS 118

RESULT 2

ADO32091
 ID ADO32091 standard; protein; 118 AA.

AC ADO32091;

XX 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

DE anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 KW heavy chain.

XX Mus musculus.

XX WO2004043344-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

DR N-PSDB; ADO32140.

XX New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.

XX Claim 5; SEQ ID NO 7; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 heavy chain
 CC variable region, which is used in an example from the present invention.

XX SQ Sequence 118 AA;

Query Match 98.4%; Score 613; DB 8; Length 118;
 Best Local Similarity 98.3%; Pred. No. 9.3e-44;
 Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQGLEWVGVIYPGNDISY 60

DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQGLEWVGVIYPGNDISY 60

QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTTVSS 118

DB 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTTVSS 118

RESULT 3

ADO32157

ID ADO32157 standard; protein; 117 AA.

XX ADO32157;

XX 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.

XX anti-CD33 antibody; epitope-binding fragment;

XX complementarity-determining region; CDR; immunoconjugate; cytostatic;

XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;

XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.

XX Mus musculus.

```

PN WO2004043344-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US032737.
XX
PR 07-NOV-2002; 2002US-0424332P.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Hoffee MG, Tavares D, Lutz RJ;
XX
DR WPI; 2004-411619/38.
XX
PT New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.
XX
XX Example 3; SEQ ID NO 73; 124pp; English.
XX
CC The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoconjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunoconjugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment; immunoconjugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunoconjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
CC amino acid sequence, which is used in an example from the present
XX invention.
XX
SQ Sequence 117 AA;
Query Match 97.8%; Score 609; DB 8; Length 117;
Best Local Similarity 98.3%; Pred. No. 2e-43;
Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
QY 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTITVTS 117
Db 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTITVTS 117
XX
RESULT 4
ADJ94605
ID ADJ94605 standard; protein; 121 AA.
XX

```

```

AC ADJ94605;
XX
DT 06-MAY-2004 (first entry)
XX
DE Chimeric anti-CD20 antibody variable heavy chain.
XX
KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Chimeric.
OS Unidentified.
XX
PN WO2003068821-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-GB000665.
XX
PR 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCA/J D.
XX
PI Hansen H, Qu Z, Goldenberg DM;
XX
DR WPI; 2003-697522/66.
DR N-PSDB; ADJ94604.
XX
PT New humanized anti-CD20 monoclonal antibody (MAb) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune diseases.
XX
PS Disclosure; Fig 2B; 106pp; English.
XX
CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC (MAb) or its antigen-binding fragment containing the complementarity
CC determining regions (CDRs) of at least one murine anti-CD20 MAb variable
CC region and the framework regions (FRs) of at least one human IV1AB
CC variable region. The antibodies of the invention are useful for
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC present amino acid sequence represents a chimeric anti-CD20 antibody
CC variable heavy chain.
XX
SQ Sequence 121 AA;
Query Match 86.4%; Score 538.5; DB 7; Length 121;
Best Local Similarity 84.3%; Pred. No. 1.7e-37;
Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;
QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
QY 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 117
Db 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 120
QY 118 S 118
Db 121 S 121
XX
RESULT 5
ADJ94607
ID ADJ94607 standard; protein; 121 AA.
XX
AC ADJ94607;
XX

```

DT	06-MAY-2004	(first entry)	
XX		Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.	
DE		humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;	
XX		IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;	
XX		thrombocytopenia; lupus; rheumatoid arthritis;	
KW		heavy chain variable region.	
KW		humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;	
KW		IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;	
KW		thrombocytopenia; lupus; rheumatoid arthritis;	
KW		heavy chain variable region.	
XX		Chimeric.	
OS		Unidentified.	
XX		WO2003068821-A2.	
PN		21-AUG-2003.	
XX		14-FEB-2003; 2003WO-GB000665.	
XX		14-FEB-2002; 2002US-0356132P.	
XX		07-OCT-2002; 2002US-0416232P.	
PR		(IMMU-) IMMUNOMEDICS INC.	
XX		(MCCA/) MCCALL J D.	
PA		Hansen H, Qu Z, Goldenberg DM;	
PA		WPI; 2003-697522/66.	
PI		New humanized anti-CD20 monoclonal antibody (Mab) that retains	
XX		substantially the B-cell and B-cell lymphoma and leukemia cell targeting	
XX		of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,	
XX		leukemia or an autoimmune diseases.	
DR		Claim 22; Fig 4A; 106pp; English.	
XX		The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody	
XX		(Mab) or its antigen-binding fragment containing the complementarity	
CC		determining regions (CDRs) of at least one murine anti-CD20 Mab variable	
CC		region and the framework regions (FRs) of at least one human IV1AB	
CC		variable region. The antibodies of the invention are useful for	
CC		diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune	
CC		disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The	
CC		present amino acid sequence represents a chimeric anti-CD20 antibody	
CC		variable heavy chain.	
XX		Sequence 121 AA;	
XX		Query Match 86.4%; Score 538.5; DB 7; Length 121;	
XX		Best Local Similarity 84.3%; Pred. No. 1.7e-37;	
XX		Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;	
Qy	1	QVQLQQPGARVVKPGASVKMSCKASGYTFTSYIHWIKQTPTGQGLEWGVYIPGNDISY 60	
Db	1	QVQLQQPGAEIVKPGASVKMSCKASGYTFTSYNMHWVKQTPTGQGLEWIGAIYIPGNDTSY 60	
Qy	61	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCYAREVRLR---YFDVWGQGTITVTS 117	
Db	61	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCYAREVRLR---YFDVWGQGTITVTS 120	
Qy	118	S 118	
Db	121	S 121	
RESULT 6			
ADJ94601			
ID	ADJ94601	standard; protein; 120 AA.	
XX			
XX	ADJ94601;		
AC			
XX	06-MAY-2004	(first entry)	
DT		Mouse anti-CD20 antibody variable heavy chain.	
XX			
DE			

FH Key Location/Qualifiers
 FT Domain 31..35
 FT /note= "Complementarity determining region (CDR) 1"
 FT Domain 50..66
 FT /note= "Complementarity determining region (CDR) 2"
 FT Domain 99..111
 FT /note= "Complementarity determining region (CDR) 3"
 XX
 PN WO2003002607-A1.
 XX
 XX 09-JAN-2003.
 XX
 PF 10-JUN-2002; 2002WO-US018512.
 XX
 PR 27-JUN-2001; 2001US-00892613.
 XX
 PA (LEUNG/) LEUNG S S.
 XX
 PI Leung SS;
 XX
 DR WPI; 2003-210245/20.
 XX
 XX New re-engineered or framework-patched immunoglobulin, useful for
 PT preparing a composition for treating cancer, preferably Non-Hodgkin's
 PT lymphoma or rheumatoid arthritis.
 XX
 PS Example 2; Fig 7a; 66pp; English.
 XX
 CC The invention relates to a novel re-engineered or framework (FR)-patched
 CC immunoglobulin, containing the heavy and/or light chain variable region
 CC (VH/VL) sequences from a parent antibody. Within these chains, at least
 CC one of the compartmentalised framework sequences, defined as FR1, FR2,
 CC FR3 and FR4 are replaced, or patched, by the corresponding framework
 CC sequences from the heavy and light chain immunoglobulin region of a
 CC different species. The FR-patched immunoglobulin binds specifically to an
 CC antigen with affinity comparable to, or within 3-fold of, that of the
 CC parent immunoglobulin. The invention discloses the process of FR-patching
 CC which is used to generate re-engineered immunoglobulin chains having one
 CC or more complementarity determining regions (CDR's) from a donor
 CC immunoglobulin and portions of framework sequences from one or more human
 CC or primate immunoglobulins. The molecules obtained demonstrate cytostatic
 CC activity as well as reduced or eliminated immunogenicity, whilst
 CC maintaining the specificity and affinity of the parent antibody. The FR-
 CC patched immunoglobulin is useful during the preparation of a composition
 CC for treating cancer, preferably Non-Hodgkin's lymphoma and also during
 CC the treatment of rheumatoid arthritis. Furthermore, the molecules of the
 CC invention may also prove useful in gene therapy. The current sequence is
 CC that of the murine anti-CD20 antibody, 1F5, VH protein of the invention
 XX
 SQ Sequence 123 AA;
 Query Match 84.9%; Score 529; DB 6; Length 123;
 Best Local Similarity 82.0%; Pred. No. 1.1e-36;
 Matches 100; Conservative 9; Mismatches 9; Indels 4; Gaps 1;
 QY 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYFGNDISY 60
 DB 1 QVQLRQFGLVLPFGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 60
 QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR-----EVRLRYFDVWGQGTITV 116
 DB 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSHYGSNYVDYFDVWGQGTITV 120
 QY 117 SS 118
 DB 121 SS 122
 RESULT 8
 AAR55215
 ID AAR55215 standard; protein; 140 AA.
 XX
 AC AAR55215;

XX 25-MAR-2003 (revised)
 DT 01-FEB-1995 (first entry)
 XX
 DB Murine variable region heavy chain from 2B8.
 XX
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 KW cell lysis.
 XX
 OS Mus musculus.
 XX
 PN WO9411026-A2.
 XX
 PD 26-MAY-1994.
 XX
 PF 12-NOV-1993; 93WO-US010953.
 XX
 PR 13-NOV-1992; 92US-00978891.
 PR 03-NOV-1993; 93US-00149099.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Rastetter WH, Hanna N, Leonard JE, Newman RA;
 PI Reff ME;
 XX
 DR WPI; 1994-183162/22.
 DR N-PSDB; AAQ65631.
 XX
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing
 PT rapid depletion of peripheral B cells, also new antibodies and
 PT hybridomas.
 XX
 PS Disclosure; Fig 5; 101pp; English.
 XX
 CC The sequence is the murine variable region heavy chain derived from
 CC murine anti-CD20 monoclonal antibody 2B8. See also AAQ65629-35. (Updated
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX
 SQ Sequence 140 AA;
 Query Match 84.3%; Score 525.5; DB 2; Length 140;
 Best Local Similarity 81.8%; Pred. No. 2.4e-36;
 Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYFGNDISY 60
 DB 20 QVQLQPGAEVWPKGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 79
 QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRL---RYFDVWGQGTITV 117
 DB 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTYYGDSYFNVWGAGTTV 139
 QY 118 S 118
 DB 140 A 140
 RESULT 9
 AAB30694
 ID AAB30694 standard; protein; 412 AA.
 XX
 AC AAB30694;
 XX
 XX 02-APR-2001 (first entry)
 DT
 DE A fusion of anti-CD20 single chain antibody/streptavidin.
 XX
 KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; B9E9.
 XX
 OS Synthetic.
 OS Streptomyces avidinii.

```
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .108
FT Peptide /note= "VL chain"
FT FT 109. .126
FT FT /note= "linker"
FT FT 127. .248
FT FT /note= "VH chain"
FT FT 249. .253
FT FT /note= "linker"
FT FT 254. .412
FT FT /note= "streptavidin"
XX
PN WO200075333-A1.
XX
PD 14-DEC-2000.
XX
XX 05-JUN-2000; 2000WO-US015595.
XX
XX 07-JUN-1999; 99US-0137900P.
PR 03-DEC-1999; 99US-0168976P.
XX
PA (NEOR-) NEORX CORP.
XX
PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX
DR WPI; 2001-091213/10.
XX
DR N-PSDB; AAC86563.
XX
PT New vector constructs for expressing genomic streptavidin fusion proteins
PT which are useful for targeting tumor cells associated with cancer, e.g.
PT adenocarcinomas.
XX
PS Example 2; Fig 11B; 100pp; English.
XX
CC The present sequence represents a fusion of an anti-CD20 single chain
CC antibody (B9E9) streptavidin. The fusion protein is expressed using
CC vectors of the invention. The specification describes vector constructs
CC for expressing streptavidin fusion proteins. The vector comprises a
CC nucleic acid encoding streptavidin or its functional variant operatively
CC linked to a promoter, and a cloning site for insertion of a second
CC nucleic acid sequence encoding a polypeptide to be fused with
CC streptavidin, interspersed between the promoter and the first nucleic acid
CC sequence. Alternatively, the vector construct comprises a nucleic acid,
CC operatively linked to a promoter, encoding a polypeptide to be fused with
CC streptavidin, and a cloning site for insertion of a second nucleic acid
CC encoding at least 129 amino acids of streptavidin or its functional
CC variant. The fusion proteins are useful for targeting tumour cells,
CC particularly tumour cells associated with cancer, e.g. adenocarcinomas or
CC hematological malignancies. The vector construct is useful for expressing
CC of streptavidin fusion proteins. In particular, these are useful as tools
CC for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC presence or absence of, or treating, a target site within a mammalian
CC host
XX
SQ Sequence 412 AA;
XX
Query Match 84.3%; Score 525.5; DB 4; Length 412;
Best Local Similarity 83.6%; Pred. No. 7e-36;
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;
QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGGLWGVVYPGNDISY 60
DB 128 QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPQGGLWIGAIYPGNGDTSY 187
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR ---YEDVWGQGTIVTV 116
DB 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAR-AQLRPNTWYFDVWGAGTIVTV 246
QY 117 SS 118
DB 247 SS 248
```

```
RESULT 10
ABJ39009
ID ABJ39009 standard; protein; 412 AA.
XX
AC ABJ39009;
XX
DT 09-OCT-2003 (first entry)
XX
DE B9E9 scFvSA fusion protein A amino acid sequence.
XX
KW Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scFvSA;
KW anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy;
KW cell-specific targeting agents; single chain; tumour; B9E9.
XX
XX Streptomyces avidinii.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .106
FT FT /note= "VL region of the fusion protein"
FT Region 107. .127
FT FT /note= "Synthetic linker region (pKOD)"
FT FT 128. .247
FT FT /note= "VH region of the fusion protein"
FT FT 248. .253
FT FT /note= "Synthetic linker region"
FT FT 254. .412
FT FT /note= "Streptavidin region of the fusion protein"
XX
PN WO2003050260-A2.
XX
PD 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US039429.
XX
XX 07-DEC-2001; 2001US-00013173.
PR 17-MAY-2002; 2002US-00150762.
PR 16-SEP-2002; 2002US-00244821.
XX
PA (NEOR-) NEORX CORP.
XX
XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
PI Dearstyne EA;
XX
DR WPI; 2003-532908/50.
DR N-PSDB; ABT43498.
XX
XX New vector construct for expressing genomic streptavidin fusion proteins
XX useful as diagnostic markers or as cell-specific targeting agents.
PS Disclosure; Fig 11B; 156pp; English.
XX
XX This invention relates to novel vector constructs for the expression of
XX streptavidin fusion proteins. Streptavidin (SA) is produced by
XX Streptomyces avidinii and specifically binds water-soluble biotin. The
XX vectors comprise a nucleic acid sequence encoding genomic streptavidin, a
XX promoter operatively linked to the nucleic acid sequence encoding an anti-
XX site for insertion of a second nucleic acid sequence encoding an anti-
XX CD25 antibody or its antigen binding fragment. The fusion proteins
XX encoded are known as single chain antibody-genomic streptavidin fusion
XX proteins (scFvSA). The vectors may have cytostatic activity when used in
XX gene therapy. The vectors may be useful in expressing genomic
XX streptavidin fusion cassettes. The fusion proteins may be used as
XX diagnostic markers or as cell-specific targeting agents. These may also
XX be used in treating tumours. The present sequence is the amino acid
XX sequence of the B9E9 single chain antibody-genomic streptavidin fusion
XX protein of the invention
SQ Sequence 412 AA;
```


Query Match 84.3%; Score 525.5; DB 6; Length 412;
 Best Local Similarity 83.6%; Pred. No. 7e-36;
 Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWGVYIPGNDISY 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 128 QVQLVQSGAEVLKPGASVKMSCKASGYTFTSYNHHWVKQTPGQGLEWIGAIYPGNGDTSY 187
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTITVTV 116
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 188 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWFYFDVWGAGTITVTV 246
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
 ||
 Db 247 SS 248
 ||

RESULT 11
 ABR55873
 ID ABR55873 standard; protein; 140 AA.
 XX AC ABR55873;
 XX DT 02-SEP-2003 (first entry)
 XX DE Anti-CD20 antibody heavy chain variable region.
 XX KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;
 XX KW antibody; mouse.
 XX OS Mus musculus.
 XX PN WO2003031464-A2.
 XX PD 17-APR-2003.
 XX PF 09-OCT-2002; 2002WO-US032263.
 XX PR 10-OCT-2001; 2001US-0328523P.
 XX PR 19-OCT-2001; 2001US-0344692P.
 XX PR 28-NOV-2001; 2001US-0334233P.
 XX PR 28-NOV-2001; 2001US-0334301P.
 XX PR 07-JUN-2002; 2002US-0387292P.
 XX PR 25-JUN-2002; 2002US-0391777P.
 XX PR 17-JUL-2002; 2002US-0396594P.
 XX PR 16-AUG-2002; 2002US-0404249P.
 XX PR 28-AUG-2002; 2002US-0407527P.

(NEOS-) NEOSE TECHNOLOGIES INC.
 De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
 WPI; 2003-449162/42.
 DR N-PSDB; ACC78895.
 XX
 XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to
 form truncated glycan, and adding or deleting glycosyl groups to a
 peptide and/or adding modifying group of a peptide to remodel the
 peptide.
 XX
 XX Example; Fig 83B; 900pp; English.

XX The invention relates to a cell-free, in vitro method of remodeling a
 CC peptide. The method involves removing a saccharyl subunit from the
 CC peptide, thus forming a truncated glycan, and contacting the truncated
 CC glycan with at least one glycosyltransferase and at least one glycosyl
 CC donor under conditions suitable to transfer at least one glycosyl donor
 CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
 CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
 CC interferon alpha peptide, interferon beta peptide, factor VIIa peptide,
 CC factor IX peptide, follicle stimulating hormone peptide, erythropoietin
 CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
 CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-P)

CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
 CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
 CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
 CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti-HER2
 CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
 CC CD20 antibody peptide, recombinant dnase peptide, anti-TNF alpha peptide,
 CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
 CC hormone (HGH) peptide, and a modifying group, where the modifying group
 CC is covalently attached to the peptide through an intact glycosyl linking
 CC group. The method is useful for a cell-free, in vitro method of
 CC remodeling the above mentioned peptides. The present sequence represents
 CC the murine anti-CD20 antibody heavy chain mature variable region
 XX

SQ Sequence 140 AA;
 Query Match 84.2%; Score 524.5; DB 6; Length 140;
 Best Local Similarity 81.8%; Pred. No. 2.9e-36;
 Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWGVYIPGNDISY 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNHHWVKQTPGQGLEWIGAIYPGNGDTSY 79
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTITVTVS 117
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGDMYFNVWGAGTITVTVS 139
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
 ;
 Db 140 A 140
 ;

RESULT 12
 ABR08394
 ID ABR08394 standard; protein; 140 AA.
 XX AC ABR08394;
 XX DT 11-JUN-2003 (first entry)
 XX DE Murine anti-CD20 antibody heavy chain variable region.
 XX KW B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VH;
 XX KW expression vector; murine; heavy chain; variable region.
 XX OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..119
 FT /label= Signal_peptide
 FT Protein 20..140
 FT /label= Mature_anti-CD20_antibody_VH_region
 XX US2002197255-A1.
 XX
 XX 26-DEC-2002.
 XX
 XX 25-JUL-2001; 2001US-00911703.
 XX
 XX 07-JUN-1995; 95US-00475813.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;
 PI Rastetter WH;
 XX WPI; 2003-352746/33.
 XX DR N-PSDB; ABX94209.
 XX
 XX Treating B cell lymphoma in humans, comprises administering
 PT immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled
 PT anti-CD20 antibodies to the human.
 XX

PS Example; Fig 5; Sipp; English.

XX The present invention relates to a method for treating B cell lymphoma.

CC The method comprises administering at a first administration period, an

CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or

CC administering, at a second administration period, a radiolabelled anti-

CC CD20 antibody, to the human subject. The invention also discloses

CC expression vectors that may be used in the method of the present

CC invention. The method is useful for treating B cell lymphoma in humans.

CC The present sequence represents murine anti-CD20 antibody heavy chain

CC variable region

XX Sequence 140 AA;

QY Query Match 84.2%; Score 524.5; DB 6; Length 140;

Best Local Similarity 81.8%; Pred. No. 2.9e-36;

Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDLISY 60

20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGIEWIGAIYPGNGDTSY 79

61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 117

80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 139

118 S 118

140 A 140

RESULT 13

ADC66270

ID ADC66270 standard; protein; 140 AA.

XX AC ADC66270;

DT 18-DEC-2003 (first entry)

XX DE Mouse anti-CD20 antibody heavy chain variable region.

XX KW immunosuppressant; cytostatic; antibody; CD20;

XX KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;

XX KW sugar chain; cancer; immune disorder.

XX OS Mus musculus.

XX WO2003055993-A1.

XX PD 10-JUL-2003.

XX PF 25-DEC-2002; 2002WO-JP013534.

XX PR 25-DEC-2001; 2001JP-00392753.

XX PR 09-APR-2002; 2002JP-00106948.

XX PR 01-NOV-2002; 2002JP-00319975.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;

XX WPI; 2003-559274/52.

XX N-PSDB; ADC66269.

XX Antibody binding to CD20 and having Fc-bound sugar chains of low fucose

XX content for treatment of cancer and immune disorders.

XX Disclosure; SEQ ID NO 14; 200pp; Japanese.

XX The invention relates to cells producing an antibody molecule

CC specifically binding to CD20 are new, in which the antibody contains N-

CC glycoside bond complex sugar chains bonded to the Fc region of the

CC antibody peptide chains, of which less than 20% have a fucose residue

CC bonded to the N-acetylglucosamine residue at the reducing end of the

CC sugar chain. The cells are used in the treatment and prevention of cancer

CC and immune disorders. This sequence corresponds to a protein used in the

CC method of the invention.

XX Sequence 140 AA;

QY Query Match 84.2%; Score 524.5; DB 7; Length 140;

Best Local Similarity 81.8%; Pred. No. 2.9e-36;

Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDLISY 60

20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGIEWIGAIYPGNGDTSY 79

61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 117

80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 139

118 S 118

140 A 140

RESULT 14

ADE85690

ID ADE85690 standard; protein; 140 AA.

XX AC ADE85690;

DT 29-JAN-2004 (first entry)

XX DE Murine immunoglobulin heavy chain variable region.

XX KW B cell lymphoma; anti-CD20; peripheral B cell; C2B8;

XX KW immunoglobulin heavy chain variable region; mouse; antibody.

XX OS Mus sp.

XX US2003147885-A1.

XX PD 07-AUG-2003.

XX PF 11-SEP-2002; 2002US-00238681.

XX PR 13-NOV-1992; 92US-00978891.

XX PR 03-NOV-1993; 93US-00149099.

XX PR 29-AUG-1997; 97US-00921060.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;

XX Rastetter WH;

XX WPI; 2003-897520/82.

XX N-PSDB; ADE85689.

XX Treating B cell lymphoma by administering an anti-CD20 antibody and at

XX least one chemotherapeutic agent.

XX Example; SEQ ID NO 11; 52pp; English.

XX The invention relates to an improved method for treating B cell lymphoma

CC comprising administering an anti-CD20 antibody. The improvement comprises

CC administering at least one chemotherapeutic agent. The antibody causes a

CC substantial depletion of peripheral B cells. The antibody is chimeric

CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.

CC This sequence represents a murine immunoglobulin heavy chain variable

CC region used in the method of the invention.

XX Sequence 140 AA;

QY Query Match 84.2%; Score 524.5; DB 7; Length 140;

	Best Local Similarity	81.8%;	Pred. No.	2.9e-36;	Matches	99; Conservative	9; Mismatches	10; Indels	3; Gaps	1;
Qy	1 QVQLQQPGAEVLKPKGASVKMCKSKASYTFTSYIIHWIKQTGGGLEWGVIPGNDDISY	60					:	: :: :	:: :	:: :
Dd	20 QVQLQQPGLLVPKGASVKMSKAGYTFTTSYNMHMVKTGPGRGLEWIGAIYPNGDTSY	79					:	: :: :	:: :	:: :
Qy	61 NQFQGKATLTADKSSTTAAYMQLSLTTSDSAVIYCAREVRLLR---	YFDVMWGOGTTVTVS 117					:	: :: :	:: :	:: :
Dd	80 NQFKGKATLTADKSSSTAAYMLSLTTSDSAVIYCARSYYYGGDWYFNVMGAGTTVTVS	139					:	: :: :	:: :	:: :
Qy	118 S 118 :						:	: :: :	:: :	:: :
Dd	140 A 140 :						:	: :: :	:: :	:: :
Qy	Search completed: May 9, 2006,	01:25:27								
Dd	Job time : 107.251 secs									

RESULT 15	
ADE73084	
ID ADE73084 standard; protein; 140 AA.	
XX AC ADE73084;	
XX AC	
XX DT 29-JAN-2004 (first entry)	
XX DE Murine FUT8-related sequence.	
XX DE	
XX KW Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial;	
XX KW Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour;	
XX KW allergy; inflammation; autoimmune disease; circulatory disorder;	
XX KW viral infection; bacterial infection; murine.	
XX OS Mus musculus.	
XX OS	
XX PN WO2003085107-A1.	
XX PN	
XX PD 16-OCT-2003.	
XX PD	
XX PF 09-APR-2003; 2003WO-JP004507.	
XX PF	
XX PR 09-APR-2002; 2002JP-00106953.	
XX PR	
XX PA (KYOW) KYOWA HAKKO KOGYO KK.	
XX PA	
XX PI Yamane N, Satoh M, Mori K, Yamano K;	
XX PI	
XX DR WPI; 2003-833570/77.	
XX DR	
XX DR N-PSDB; ADE73069.	
XX DR	
XX PT Cells with reduced or absent alpha 1,6-fucosyltransferase activity for	
XX PT treatment of tumors, allergy, inflammation, autoimmune disease,	
XX PT circulatory disorders, and viral and bacterial infection.	
XX PT	
XX PS Example 6; Page 165-166; 187pp; Japanese.	
XX PS	
XX CC The present invention relates to cells with modified sugar chain	
XX CC modifying enzyme activity. The enzyme activity of binding the 1-position	
XX CC of fucose to the 6-position of an N-acetylglucosamine at the reducing end	
XX CC of a complex N-glycoside linked sugar chain via an alpha-bond is absent	
XX CC or less than in the parent cell. The sugar chain modifying enzyme is	
XX CC preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-	
XX CC ADE73056). The invention is useful for the treatment and prevention of	
XX CC tumours, allergy, inflammation, autoimmune disease, circulatory	
XX CC disorders, and viral and bacterial infection. The present sequence was	
XX CC used in an example from the invention.	
XX CC	
XX SQ Sequence 140 AA;	
XX SQ	
Query Match	84.2%; Score 524.5; DB 7; Length 140;
Best Local Similarity	81.8%; Pred. No. 2.9e-36;
Matches 99; Conservative	9; Mismatches 10; Indels 3; Gaps 1;
QY	1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKRPGQGLEWVGVIYPCGNDISY 60

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.8788 Seconds
(without alignments)
635.031 Million cell updates/sec

Title: US-10-700-632-9
Perfect score: 623
Sequence: 1 QVQLQQPGAEVVKPGASVKM.....EVLRLYFDVWGQGTITVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	79.6	120	2 B22769	Ig heavy chain V r
2	486.5	78.1	119	2 PL0089	Ig heavy chain V r
3	486	78.0	118	2 S38717	Ig heavy chain V r
4	483.5	77.6	138	2 E32513	Ig heavy chain pre
5	482.5	77.4	120	2 S25175	Ig heavy chain V r
6	482.5	77.4	136	2 PL0208	Ig heavy chain pre
7	479.5	77.0	138	2 S21810	Ig heavy chain V r
8	478	76.7	120	2 G28195	Ig heavy chain V r
9	477	76.6	115	2 A54378	Ig heavy chain V r
10	472	75.8	101	2 S42184	Ig gamma chain V r
11	472	75.8	101	2 S42179	Ig gamma chain V r
12	472	75.8	102	2 S42180	Ig gamma chain V r
13	471	75.6	131	2 S66537	Ig heavy chain V r
14	470.5	75.5	117	1 MHMSJ5	Ig heavy chain V r
15	470.5	75.5	123	2 S20846	Ig heavy chain V r
16	470	75.4	139	1 MHMS18	Ig heavy chain pre
17	470	75.4	287	4 PC4402	peB leader/Ig hea
18	468	75.1	116	2 S53751	antibody Fab Jel 1
19	468	75.1	120	2 F28195	Ig heavy chain V r
20	468	75.1	135	2 A30577	Ig heavy chain pre
21	467	75.0	133	2 PC1155	Ig heavy chain pre
22	467	75.0	137	1 G2MS43	Ig heavy chain pre
23	466.5	74.9	246	2 S38950	Ig gamma chain - m
24	466.5	74.9	446	2 S40295	Ig gamma-2a chain
25	466	74.8	120	2 S41394	Ig heavy chain V r
26	466	74.8	141	2 A39276	Ig heavy chain pre
27	464.5	74.6	117	1 MHMS4E	Ig heavy chain V r
28	464.5	74.6	140	2 T01407	Ig heavy chain (my
29	462	74.2	115	2 C27563	Ig heavy chain V r

```

30      462      74.2      141      2      JL0076      Ig heavy chain pre
31      450      73.8      115      2      PL0238      Ig heavy chain V r
32      459.5      73.8      140      2      PH1482      Ig heavy chain V r
33      458.5      73.6      140      2      PH1484      Ig heavy chain V r
34      458      73.5      139      2      A27609      Ig heavy chain pre
35      457.5      73.4      119      2      S20640      Ig heavy chain V r
36      457      73.4      119      2      A24672      Ig heavy chain pre
37      457      73.4      137      2      F29380      Ig heavy chain pre
38      456.5      73.3      117      2      S03305      Ig heavy chain V r
39      456.5      73.3      118      2      S38565      Ig heavy chain V r
40      455.5      73.1      116      2      S55542      Ig heavy chain V r
41      454      72.9      117      2      S55541      Ig heavy chain V r
42      454      72.9      120      1      MHMS15      Ig heavy chain V r
43      454      72.9      139      2      PS0024      Ig heavy chain pre
44      453.5      72.8      140      2      PH1489      Ig heavy chain V r
45      453      72.7      117      2      S25176      Ig heavy chain V r

```

ALIGNMENTS

RESULT 1

B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Dildrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: B22769
A:Molecule type: protein
A:Residues: 1-120
A:Cross-references: UNIPARC:UPI0000176B76
A:Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2
A:Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 496; DB 2; Length 120;
Best Local Similarity 77.5%; Pred. No. 2.5e-37;
Matches 93; Conservative 12; Mismatches 13; Indels 2; Gaps 1;

```

Qy      1      QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYPGNDISY 60
Db      1      QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYMHMWKQRPQGLEWIGRIHPSDSTNY 60

Qy      61      NQKFGKATLTADKSTTAYMQLSLTSEDNAVYVCAR--EVLRLYFDVWGQGTITVTVSS 118
Db      61      NQKFGKATLTADKSTTAYMQLSLTSEDNAVYVCAR--EVLRLYFDVWGQGTITVTVSS 120

```

RESULT 2

PL0089
Ig heavy chain V region (12S18-1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
R:Meek, K.; Hasegawa, C.; Pollok, B.; Alkan, S.S.; Braith, M.; Slaoui, M.; Urbain, J.;
J. Exp. Med. 169, 519-533, 1989
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Abs are
A:Reference number: PL0080; MUID:89094248; PMID:2492056
A:Accession: PL0089
A:Molecule type: mRNA
A:Residues: 1-119
A:Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:G51591; PIDN:CAA414
A:Note: the sequences shown here are from the VH region of an antiidiotypic monoclonal ant
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 486.5; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 1.8e-36;
Matches 92; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAR-EVRLRYFDVWGQGTITVTVSS 118
DB 61 NEKFKSKATLTVDTSSTAYMQLSLTSDSDSAVYVCARNEGVAWYFDVWGQGTITVTVSS 119

RESULT 3
S38717
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38717
R:Cimanis, A. Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38717
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <CIM>
A:Cross-references: UNIPARC:UPI0000117541; EMBL:X76020; NID:g416099; PIDN:CAAS3607.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 486; DB 2; Length 118;
Best Local Similarity 77.1%; Pred. No. 1.9e-36;
Matches 91; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60
DB 1 QDQLQQSGDPLVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAREVRLRYFDVWGQGTITVTVSS 118
DB 61 NDKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCARENGFNFYFDVWGQGTITVTVSS 118

RESULT 4
E32513
Ig heavy chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C:Accession: E32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1998
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: E32513
A:Molecule type: DNA
A:Residues: 1-138 <KOP>
A:Cross-references: UNIPARC:UPI0000114D9D; GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 483.5; DB 2; Length 138;
Best Local Similarity 75.8%; Pred. No. 3.8e-36;
Matches 91; Conservative 15; Mismatches 11; Indels 3; Gaps 2;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60
DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 79

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAREVRLRYF-DVWGQGTITVTVSS 118

DB 80 NEKFKSKATLTVDTSSTAYMQLSLTSDSDSAVYCARRL-YRYAMDYWGQGTSTVTVSS 138

RESULT 5
S25175
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25175
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MON>
A:Cross-references: UNIPARC:UPI00001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 482.5; DB 2; Length 120;
Best Local Similarity 75.8%; Pred. No. 4e-36;
Matches 91; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAREV--RLRYFDVWGQGTITVTVSS 117
DB 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAREKITDDYNYFDVWGQGTITVTVSS 120

RESULT 6
PL0208
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C:Accession: PL0208
R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reaction
A:Reference number: PL0207; MUID:90309764; PMID:1973259
A:Accession: PL0208
A:Molecule type: mRNA
A:Residues: 1-136 <SOU>
A:Cross-references: UNIPARC:UPI0000176C6F
A:Experimental source: hybridoma cell E225
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:1-19/Domain: signal sequence #status predicted <SIG>
P:34-117/Domain: immunoglobulin homology <IMM>
P:50-54/Region: complementarity-determining 1
P:59-85/Region: complementarity-determining 2
P:118-125/Region: complementarity-determining 3
P:118-121/Region: D region
P:122-136/Region: JH region

Query Match 77.4%; Score 482.5; DB 2; Length 136;
Best Local Similarity 74.6%; Pred. No. 4.6e-36;
Matches 88; Conservative 17; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 60
DB 20 QVQLQPGSELVVKPGASVKMSCKASGYTFTSYTHWIKQTQPGGLEWGVYIPGNDDISY 79

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSDSAVYVCAREVRLRYFDVWGQGTITVTVSS 118
DB 80 DEKFKSKATLTVDTSSTAYMQLSLTSDSDSAVYVCARGLAF-YFDHWGQGTITVTVSS 136

RESULT 7

A;Reference number: A54378; MUID:94165109; PMID:7509814
A;Accession: A54378
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <AGA>
A;Cross-references: UNIPARC:UPI0000176E3F; GB:S68981; NID:Q545744; PIDN:AAB30095.1; PID:15-98/Domain: immunoglobulin homology <IMM>
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144172, NCBIPI:144173)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 477; DB 2; Length 115;
Best Local Similarity 75.7%; Pred. No. 1.2e-35;
Matches 87; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPTGGGLEWGVVYPCGDDISY 60
Db 1 EVQLQSGPELVKPGASVSRISCKASGYTFTSYTHWIKQRPQGLEWIGVYPCGNGTKY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSADVYFCAREVRLRYFDVWGQGTITV 115
Db 61 NEKFKGATLTADKSSSTAYMQLSSLTSDSADVYFCARSSGGYLGWVGQGTITL 115

RESULT 10
S42184
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 06-Jun-1997
C;Accession: S42184
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spleen
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42184
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <MOJ>
A;Cross-references: UNIPARC:UPI0000176E59; EMBL:Z25457
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 472; DB 2; Length 101;
Best Local Similarity 89.7%; Pred. No. 2.9e-35;
Matches 87; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 VQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPTGGGLEWGVVYPCGDDISYN 61
Db 2 VQLQQGAEVLKPGASVKMSCKASGYTFTSYNMHWVKQTPTGGGLEWIGVYPCGNGDTSYN 61

QY 62 QKFGKATLTADKSSSTAYMQLSSLTSDSADVYFCAR 98
Db 62 QKFGKATLTADKSSSTAYMQLSSLTSDSADVYFCAR 98

RESULT 11
S42179
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42179
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spleen
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42179
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <MOJ>
A;Cross-references: UNIPARC:UPI000011655F; EMBL:Z25447; NID:9407816; PIDN:CAA80934.1; PID:15-98/Domain: immunoglobulin homology <IMM>

THIS PAGE BLANK (uspto)

01 FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DT VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
 DE Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
 GN

✓

Query Match 77.7%; Score 484; DB 2; Length 143;
 Best Local Similarity 76.3%; Pred. No. 7.4e-44;
 Matches 90; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 DB 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 QY 61 NQKFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118
 DB 61 NQKFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118

RESULT 5
 Q5BJ22 RAT PRELIMINARY; PRT; 458 AA.
 ID Q5BJ22 RAT PRELIMINARY; PRT; 458 AA.
 AC Q5BJ22;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DB LOC367586 protein.
 GN Names=LOC367586;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=101116;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Guichard J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC ENMBL; BC091272; AAH91272.1; -; mRNA.
 DR SNR; Q5BJ22; 21-454.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 KW Immunoglobulin domain; Repeat.
 SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 76.8%; Score 478.5; DB 2; Length 458;
 Best Local Similarity 76.9%; Pred. No. 1.2e-42;
 Matches 93; Conservative 9; Mismatches 12; Indels 7; Gaps 0;

QY 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 DB 20 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 79
 QY 61 NQKFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 117
 DB 80 NQKFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 135

RESULT 6
 Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
 ID Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
 AC Q924R8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DB VHI86.2-D-J-C mu protein (Fragment).
 GN Name=VHI86.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RX PubMed=3135311;
 RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
 RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
 C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
 specific V genes as the original antigen.";
 RL J. Immunol. 141:779-784 (1988).
 DR ENMBL; AB067781; BAB63266.1; -; mRNA.
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR HSSP; P01751; 1A6W.
 DR SNR; Q924R8; 1-137.
 DR ENMBL; ENSMUSG00000021155; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.

Query Match 77.7%; Score 484; DB 2; Length 143;
 Best Local Similarity 76.3%; Pred. No. 7.4e-44;
 Matches 90; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 DB 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 QY 61 NQKFGQKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLRYFDVWGQGTFTVTS 118
 DB 61 NEKFKSKATLTADKSPSTAYMQLSSLTSDSAVYYCAREVRYEYFDVWGVTGTTVTS 118

RESULT 5
 Q5BJ22 RAT PRELIMINARY; PRT; 458 AA.
 ID Q5BJ22 RAT PRELIMINARY; PRT; 458 AA.
 AC Q5BJ22;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DB LOC367586 protein.
 GN Names=LOC367586;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=101116;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Guichard J., Schmitt J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC ENBL; BC091272; AAH91272.1; -; mRNA.
 DR SMR; Q5BJ22; 21-454.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 KW Immunoglobulin domain; Repeat.
 SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 76.8%; Score 478.5; DB 2; Length 458;
 Best Local Similarity 76.9%; Pred. No. 1.2e-42;
 Matches 93; Conservative 9; Mismatches 12; Indels 7; Gaps 0;

QY 1 QVQLQPGAEVAVKPGASVKMSCKASGYTFTSYVHMKOTPGGLEWGVYIPGNDLISY 60
 DB 20 QVQLQSGAEVAVKPGASVKISCKASGYTFTNIDHMKOTPGNGLEWGVYIPGNGTKY 79
 QY 61 NQKFGQKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLRYF---DVWGQGTFTVTS 117
 DB 80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD---YFDGYDWGQGVMTVS 135

RESULT 6
 Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
 ID Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
 AC Q924R8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DB VHI86.2-D-J-C mu protein (Fragment).
 GN Name=VHI86.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RX PubMed=3135311;
 RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
 RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
 RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
 RT specific V genes as the original antigen.";
 RL J. Immunol. 141:779-784(1988).
 DR ENBL; AB067781; BAB63266.1; -; mRNA.
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q924R8; 1-137.
 DR ENBL; ENSMUSG00000021155; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.

```
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460FLDFLFB7538 CRC64;

Query Match
Best Local Similarity 76.6%; Score 477.5; DB 2; Length 146;
Matches 90; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLWVGVIYPGNDDISY 60
Db 1 QVQLQQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLWVGVIYPGNDDISY 60

Qy 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVVCAREV---RLRYEDVWGQGTFTVVS 117
Db 61 NEKFSKATLTVDKPSSTAYMQLSLTSDSAVVCARSYYGSSLIYFDYWGQGTFTVVS 120

Qy 118 S 118
Db 121 S 121

RESULT 7
Q921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q921C4
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78801; AAD00293.1; -; mRNA.
DR SMR; Q921C4; 1-118.
DR InterPro; IPR007110; IG-like.
DR Ensemble; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 908ECS59D31EC4FC CRC64;

Query Match
Best Local Similarity 76.6%; Score 477; DB 2; Length 118;
Matches 88; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QVQLQQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLWVGVIYPGNDDISY 60
Db 1 QVQLQQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLWVGVIYPGNDDISY 60

Qy 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVVCAREVRLRYEDVWGQGTFTVVS 118
Db 61 TQKFRGKATLTADKSSSTAYMQLSLTSDSAVVCARRTVGGYFDYWGQGTFTVVS 118

RESULT 8
Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
ID Q8VCX7_MOUSE
```

```
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2464031;
RA Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
RT antigen-binding of monoclonal antibodies to alpha(1----6)dextran."
RL J. Immunol. 142:888-893(1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR PIR; C30562; C30562.
DR HSP; P01751; I46W.
DR Ensemble; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 4.
```

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match
Best Local Similarity 76.2%; Score 475; DB 2; Length 613;
Matches 88; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQLEWVGVIYFGNDISY 60
DB 20 QVLOQPGAEVVKPGASVKMSCKATGTYTSSYIHWIKQTPGGQLEWVGVIYFGNDISY 118
QY 61 NQFOGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFVWVGTTVTSS 118
DB 80 NEKFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFVWVGTTVTSS 137

RESULT 9
Q924R7 MOUSE
ID Q924R7_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924R7_MOUSE PRELIMINARY; PRT; 143 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Names=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAR idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784 (1988).
[3]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3211160;
RA Kaartinen M., Rocca-Serra J., Makela O.;
RT "Combinatorial association of V genes: one VH gene codes for three
RT non-cross-reactive monoclonal antibodies each specific for a different
RT antigen (phoxazolone, NP or gat).";
RL Mol. Immunol. 25:859-865 (1988).
DR EMBL; AB067782; BAB63267.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; JLO078; JLO078.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R3; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

Query Match
Best Local Similarity 76.1%; Score 474; DB 2; Length 143;
Matches 88; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQLEWVGVIYFGNDISY 60
DB 20 QVLOQPGAEVVKPGASVKMSCKATGTYTSSYIHWIKQTPGGQLEWVGVIYFGNDISY 118
QY 61 NQFOGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFVWVGTTVTSS 118
DB 80 NEKFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFVWVGTTVTSS 137
```

```

FT  NON_TER      1      145
SQ  SEQUENCE      145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;

Query Match      75.6%; Score 471; DB 2; Length 145;
Best Local Similarity 75.0%; Pred. No. 1.9e-42;
Matches 90; Conservative 12; Mismatches 16; Indels 2; Gaps 1;

QY  1  QVQLQQPGAEVVKPGASVKMSCKASGTYFTSYIHWIKQTQPGQGLGWGVYPGNDDISY 60
DB  1  QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVQKQRPGRGLEWIGRIDPNSSGGTKY 60

QY  61  NQPKQKATLTADKSSSTAYNQLSSLTSEDSAVVYCARV--RLRYFDVWGQGTGTTVTYSS 118
DB  61  NERPKSKATLTVDKPSSTAYNQLSSLTSEDSAVVYCARGLYDGNWYFDVWGQGTGTTVTYSS 120

RESULT 11
ID  Q6PJB2 MOUSE PRELIMINARY; PRT; 465 AA.
AC  Q6PJB2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Hypothetical protein.
OS  Names=Igh-1a;
GN  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=Czech II;
RC  TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC  Expression driven by an MMTV-LTR enhancer.;
RX  MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA  Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=Czech II;
RC  TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC  Expression driven by an MMTV-LTR enhancer.;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC018280; AAH18280.1; -, mRNA.
DR  HSSP; P01865; 1KB5.
DR  SMR; Q6PJB2; 20-461.
DR  MGI; MGI:96443; Igh-1a.
DR  GO; GO:0003823; P:antigen binding; IEA.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG MHC.

```


QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
 Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
 QY 61 NQKFOGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTIVTVSS 118
 Db 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCARD-RYWFYDWGAGTIVTVSS 117

RESULT 13

Q924Q1_MOUSE
 ID Q924Q1_MOUSE PRELIMINARY; PRT; 142 AA.
 AC Q924Q1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE V23-D-J-C mu protein (Fragment).
 GN Name=AB069917; Synonyms=V23-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RC Kozono Y., Kozono H., Azuma T.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 RP [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=3135311;
 RA Corbet S., Hirn M., Roth C., These J., Fougereau M., Schiff C.;
 RT "Allogeneic manipulation of the GAT idiotypic cascade: Immunization of
 RT C57BL/6 mice by BAUB/c anti-idiotypes stimulates similar strain-
 RT specific V genes as the original antigen";
 RL J. Immunol. 141:779-784(1988).
 RP [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=9238144; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZW)F1 mice";
 RL J. Exp. Med. 176:761-779(1992).
 DR EMBL; AB069913; BAB63929.1; -; mRNA.

DR PIR; F33932; F33932.
 DR PIR; I28833; I28833.
 DR PIR; PH0985; PH0985.
 DR PIR; PH1155; PH1155.
 DR PIR; PH1156; PH1156.
 DR PIR; PH1157; PH1157.
 DR PIR; PH1158; PH1158.
 DR HSP; P01751; IAA6W.
 DR SMR; Q924Q1; 1-128.
 DR Ensembl; ENSMUSG0000021155; Mus musculus.
 DR MGI; MGI:3576502; AB069917.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 142
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4138B CRC64;

Query Match 75.5%; Score 470.5; DB 2; Length 142;
 Best Local Similarity 75.4%; Pred. No. 2.1e-42;
 Matches 89; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
 Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
 QY 61 NQKFOGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTIVTVSS 118
 Db 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCARR-GWEAMDYWGQGTIVTVSS 117

RESULT 14

Q7THK1_MOUSE
 ID Q7THK1_MOUSE PRELIMINARY; PRT; 470 AA.
 AC Q7THK1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein AI324046.
 GN Name=AI324046;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055910; AAH55910.1; -; mRNA.
 DR HSP; P01865; IKB5.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein, Immunoglobulin domain.

SQ SEQUENCE 470 AA; 51728 MW; 6D90E4DF896BB090 CRC64;
 Query Match 75.5%; Score 470.5; DB 2; Length 470;
 Best Local Similarity 72.7%; Pred. No. 8.7e-42;

Matches 88; Conservative 14; Mismatches 16; Indels 3; Gaps 1;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
20 EVQLQSGPELVKPGASVKISCKASGYFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 79
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAR---EVRLRYFDVWGQGTIVTVSS 117
80 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYYCARYYSGSYFDVWGAGTIVTVSS 139
QY 118 \$ 118
Db 140 \$ 140

RESULT 15
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
CC making antibodies to the haptan (4-hydroxy-3-nitrophenyl)acetyl
CC (NpB antibodies).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00529; AAA38170.1; -; mRNA.
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; X-ray; H=20-139.
DR PDB; 1A6V; X-ray; H/I/J=20-139.
DR PDB; 1A6W; X-ray; H=20-139.
DR PDB; 1NGP; X-ray; H=20-139.
DR PDB; 1NGQ; X-ray; H=20-139.
DR PDB; 1NOB; X-ray; A/C=20-139.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT REGION 20 49
FT REGION 50 54
FT REGION 55 58
FT REGION 69 85
FT REGION 86 117
FT REGION 118 124
FT REGION 125 139
FT DISULFID 41 115
FT NON_TER 139 139
FT STRAND 22 24
Ig heavy chain V region B1-8/186-2.
Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
D segment.
JH2 segment.
By similarity.

FT STRAND 28 31
FT TURN 33 34
FT STRAND 37 44
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
Query Match 75.4%; Score 470; DB 1; Length 139;
Best Local Similarity 74.2%; Pred. No. 2.3e-42;
Matches 89; Conservative 12; Mismatches 17; Indels 2; Gaps 1;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60
20 QVQLQPGAEVVKPGASVKLSCKASGYFTSYIHWIKQTPGQGLEWIGRIDPNSGTTY 79
Db
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAR---EVRLRYFDVWGQGTIVTVSS 118
80 NQKFGKATLTVDKSPSTAYMQLSLTSDSAVYYCARYYSGSYFDVWGQGTIVTVSS 139
Search completed: May 9, 2006, 01:32:35
Job time : 109.039 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 26.5628 Seconds
(without alignments)
367.271 Million cell updates/sec

Title: US-10-700-632-9
Perfect score: 623
Sequence: 1 QVQLQQPGAEVVRKPGASVKM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	84.2	140	2	US-08-475-815B-11
2	524.5	84.2	470	2	US-09-238-741-4
3	516.5	82.9	140	1	US-08-476-275-6
4	516.5	82.9	140	2	US-08-475-813-6
5	502	80.6	118	2	US-08-766-350B-48
6	501.5	80.5	121	2	US-08-579-378A-7
7	501.5	80.5	121	4	PCT-US93-11612-7
8	501.5	80.5	140	4	PCT-US93-11612-4
9	498	79.9	140	2	US-09-724-138-44
10	498	79.9	140	2	US-09-630-198-44
11	495	79.5	273	1	US-08-403-853-18
12	493.5	79.2	140	2	US-08-579-378A-4
13	492	79.0	257	2	US-09-419-788-113
14	490.5	78.7	135	1	US-08-860-174A-4
15	490.5	78.7	274	1	US-08-860-174A-12
16	481.5	77.3	119	2	US-10-194-975-121
17	480.5	77.1	119	1	US-08-553-497A-12
18	479.5	77.0	117	2	US-09-157-370-2
19	478.5	76.8	288	2	US-09-423-439-38
20	478.5	76.8	673	2	US-09-423-439-32
21	474.5	76.2	445	1	US-08-353-400-33
22	474.5	76.2	464	1	US-08-353-400-36
23	473.5	76.0	119	2	US-08-881-037-60
24	473.5	76.0	119	2	US-08-881-037-62
25	473	75.9	117	2	US-09-065-059-15
26	473	75.9	117	2	US-08-913-555-15
27	473	75.9	269	1	US-08-428-257A-72

28	473	75.9	269	1	US-08-491-988-3	Sequence 3, Appli
29	473	75.9	402	1	US-08-491-988-9	Sequence 9, Appli
30	473	75.9	415	1	US-08-491-988-7	Sequence 7, Appli
31	473	75.9	435	1	US-08-491-988-5	Sequence 5, Appli
32	472.5	75.8	119	2	US-08-881-037-63	Sequence 63, Appli
33	472	75.8	122	1	US-08-236-520-9	Sequence 9, Appli
34	472	75.8	122	4	PCT-US95-05262-9	Sequence 9, Appli
35	471.5	75.7	143	1	US-08-236-520-7	Sequence 7, Appli
36	471.5	75.7	143	4	PCT-US95-05262-7	Sequence 7, Appli
37	470.5	75.5	140	1	US-07-946-421-24	Sequence 24, Appli
38	470	75.4	114	2	US-09-344-587-10	Sequence 10, Appli
39	470	75.4	122	2	US-10-092-246-10	Sequence 10, Appli
40	470	75.4	122	2	US-10-092-246-11	Sequence 11, Appli
41	470	75.4	122	2	US-10-096-246A-10	Sequence 10, Appli
42	470	75.4	122	2	US-10-096-246A-11	Sequence 11, Appli
43	469.5	75.4	119	2	US-08-881-037-61	Sequence 61, Appli
44	469	75.3	139	2	US-09-269-921-105	Sequence 105, App
45	468.5	75.2	119	2	US-09-438-954-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1
US-08-475-815B-11
; Sequence 11, Application US/08475815B
; Patent No. 6399061
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```
; MOLECULE TYPE: protein
US-08-475-815B-11

Query Match      84.2%; Score 524.5; DB 2; Length 140;
Best Local Similarity 81.8%; Pred. No. 1.2e-41;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGGLWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGGLWGVYIPGNDISY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFGKATLTADKSTTAYMQLSSITSDSAVYICAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFGKATLTADKSSSTAYMQLSSITSDSAVYICAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
   :
Db 140 A 140

RESULT 2
US-09-238-741-4
; Sequence 4, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238,741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match      84.2%; Score 524.5; DB 2; Length 470;
Best Local Similarity 81.8%; Pred. No. 4.4e-41;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGGLWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGGLWGVYIPGNDISY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFGKATLTADKSTTAYMQLSSITSDSAVYICAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFGKATLTADKSSSTAYMQLSSITSDSAVYICAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
   :
Db 140 A 140

RESULT 3
US-08-476-275-6
; Sequence 6, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted

; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigens for the Treatment of B-Cell Lymphoma
```

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince St.
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 Zip: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,813
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/149,099
 FILING DATE: 03-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/978,891
 FILING DATE: 13-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-158
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 140 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PS-08-475-813-6

Query Match	82.9%;	Score	516.5;	DB	2;	Length	140;
Best Local Similarity	81.0%;	Pred. No.	6.5e-41;				
Matches	98;	Conservative	9;	Mismatches	11;	Indels	3;
Gaps	1;						

QY	1	QVQLQPGAEVVKPGASVKMSCKASGYFTSYTHWIKOTPGGLEWGVVYPGNDITSY	60
DBb	20	QVQLQPGAEVLVKAGASVKMSCKASGYFTSYNNHWIKOTPGGLEWGAIIYPGNDITSY	79
QY	61	NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVYYCAREVRLR---	117
DBb	80	NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS	139
QY	118	S	118
DB	140	A	140

RESULT 5
US-08-766-350B-48
; Sequence 48, Application US/08766350B
; Patent No. 6949244
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; OF USE THEREOF
; 11D10 AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018

```

;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA: US/08/766,350B
;   APPLICATION NUMBER: US/08/766,350B
;   FILING DATE: 13-Dec-1996
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Polizzi, Catherine M.
;     REGISTRATION NUMBER: 40,130
;     REFERENCE/DOCKET NUMBER: 30414-20003.21
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 813-5600
;     TELEFAX: (415) 494-0792
;     TELEX: 706141
;
; INFORMATION FOR SEQ ID NO: 48:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 118 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 48:
;
; US-08-766-350B-48
;
; Query Match      80.6%; Score 502; DB 2; Length 118;
; Best Local Similarity 78.8%; Pred. No. 1.2e-39;
; Matches 93; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
;
; QY      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTGGGLEHWGVYIPGNDISY 60
;         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
;         1 QVQLQQSGNELVPGASVKMSCKASGYTFTSYIHWIKQTGGGLEHWIKGALYIPGNDTNY 60
;
; Db
;
; QY      61 NQKPGKATLTADKSTTAYMOLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTYSS 118
;
; Db      61 NQKPGKATLTADTSSSTAYMOLSLTSDSAVYFCARGXXXGAMDYWGQGTFTVTYSS 118

```

RESULT 6
US-08-579-378A-7
; Sequence 7, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-579-378A-7

Query Match      80.5%; Score 501.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.4e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
Db 1 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVHMKQKPGQGLEWGIYIPYNDGTY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREV---RLRYFDVWGQGTITVTS 117
Db 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREYGNVYRFDVWGAGTITVTS 120

QY 118 S 118
Db 121 S 121

RESULT 7
PCT-US93-11612-7
; Sequence 7, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: PCT/US93/11612
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11612-4

Query Match      80.5%; Score 501.5; DB 4; Length 140;
Best Local Similarity 77.7%; Pred. No. 1.6e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
Db 20 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVHMKQKPGQGLEWGIYIPYNDGTY 79
```

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11612-7

Query Match      80.5%; Score 501.5; DB 4; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.4e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
Db 1 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVHMKQKPGQGLEWGIYIPYNDGTY 60

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREV---RLRYFDVWGQGTITVTS 117
Db 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREYGNVYRFDVWGAGTITVTS 120

QY 118 S 118
Db 121 S 121

RESULT 8
PCT-US93-11612-4
; Sequence 4, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: PCT/US93/11612
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11612-4

Query Match      80.5%; Score 501.5; DB 4; Length 140;
Best Local Similarity 77.7%; Pred. No. 1.6e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
Db 20 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVHMKQKPGQGLEWGIYIPYNDGTY 79
```



```

; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-4

Query Match          79.2%; Score 493.5; DB 2; Length 140;
Best Local Similarity 76.9%; Pred. No. 9.1e-39;
Matches 93; Conservative 12; Mismatches 13; Indels 3; Gaps 1

QY 1 QVQLQQPGASVWVKGASVKMSCKRASGYTFTSYTHWIKQTIPGQGLEWGVYIPGNDITSY 60
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 20 EVQLQQSGPDLVRFASVWVKGASVKMSCKRASGYTFTSYVHWVWVKQKPGQGLEWIGYIYPNDGTKY 79
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 61 NQPFQGHATLTADKSSSTAYMQLSSLTSEDSAVNYCAREV---RLRVPDVKGGQGTITVTS 117
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 80 NEKPFKGAATLTDSKSSSTAYMQLSSLTSEDSAVNYCAREEYGNVYRVFVWVGAGTTVTS 139
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 118 S 118
Db 140 S 140

RESULT 13
US-09-419-788-113

```

```

; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: Resistance
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-113

Query Match          79.0%; Score 492; DB 2; Length 257;
Best Local Similarity 78.8%; Pred. No. 2.4e-38;
Matches 99; Conservative 10; Mismatches 9; Indels 6; Gaps 1

Qy      1 QVQLQQPGAEEVVKPGASVKMSCKASGYTFTSYIHWIKQTQCGGLEWGVYIPGNDDISY 60
Db      3 EVQLQQSGAEIVKPGASVKMSCKASGYTFTNYNMHWVKQTQCGGLEWIGAIYPRNGDTSY 62
Qy      61 NKPFGQKATLTADKSSITAYMQLSSLTSDSAVVYCAREVLRFVDVWGQGTTVTVSS 118

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 88.6277 Seconds
(without alignments)
556.303 Million cell updates/sec

Title: US-10-700-632-9
Perfect score: 623
Sequence: 1 QVQLQPGAEVVKPGASVKRM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pgp:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pgp:*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pgp:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	118	5	US-10-700-632-9
2	613	98.4	118	5	US-10-700-632-7
3	609	97.8	117	5	US-10-700-632-73
4	538.5	86.4	121	4	US-10-366-709-39
5	533.5	85.6	120	4	US-10-366-709-35
6	525.5	84.3	412	4	US-10-013-173-6
7	525.5	84.3	412	4	US-10-150-762-6
8	525.5	84.3	412	4	US-10-244-821-6
9	524.5	84.2	140	4	US-10-238-681-11
10	524.5	84.2	140	4	US-10-411-037-62
11	524.5	84.2	140	4	US-10-411-026-62
12	524.5	84.2	140	4	US-10-410-962-62
13	524.5	84.2	140	4	US-10-411-049-62
14	524.5	84.2	140	4	US-10-327-663-14
15	524.5	84.2	140	4	US-10-410-930-62
16	524.5	84.2	140	4	US-10-410-997-62
17	524.5	84.2	140	4	US-10-411-012-62
18	524.5	84.2	140	4	US-10-287-994-62
19	524.5	84.2	140	4	US-10-410-913-62
20	524.5	84.2	140	5	US-10-723-003-36
21	524.5	84.2	140	5	US-10-410-980-62
22	524.5	84.2	140	5	US-10-410-897-62
23	524.5	84.2	140	5	US-10-492-261-62
24	524.5	84.2	140	6	US-11-004-639-36
25	524.5	84.2	368	5	US-10-880-028-47
26	524.5	84.2	368	5	US-10-880-320-47
27	524.5	84.2	451	5	US-10-822-231-4

28	524.5	84.2	451	5	US-10-822-231-5	Sequence 5, Appli
29	524.5	84.2	470	5	US-10-723-003-40	Sequence 40, Appli
30	524.5	84.2	470	6	US-11-019-180-4	Sequence 4, Appli
31	524.5	84.2	470	6	US-11-004-639-40	Sequence 40, Appli
32	524.5	84.2	470	6	US-10-723-003-44	Sequence 44, Appli
33	524.5	84.2	470	6	US-11-004-639-44	Sequence 44, Appli
34	524.5	84.2	470	6	US-10-723-003-46	Sequence 46, Appli
35	524.5	84.2	470	6	US-11-004-639-46	Sequence 46, Appli
36	524.5	84.2	470	6	US-10-723-003-48	Sequence 48, Appli
37	524.5	84.2	470	6	US-11-004-639-48	Sequence 48, Appli
38	521.5	83.7	423	4	US/10/013	Sequence 8, Appli
39	521.5	83.7	423	4	US/10/150	Sequence 8, Appli
40	521.5	83.7	423	4	US/10/244	Sequence 8, Appli
41	517.5	83.1	121	5	US-10-917-599-1	Sequence 1, Appli
42	516.5	82.9	140	3	US-09-905-928-6	Sequence 6, Appli
43	516.5	82.9	140	4	US-10-096-964-6	Sequence 6, Appli
44	516.5	82.9	140	5	US-10-956-039-6	Sequence 6, Appli
45	512	82.2	122	5	US-10-917-599-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9

Query Match	100.0%	Score 623;	DB 5;	Length 118;
Best Local Similarity	100.0%	Pred. No. 1.1e-46;		
Matches 118;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHNIKPTPGQGLEWGVYIPGNDISY 60		
Db	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHNIKPTPGQGLEWGVYIPGNDISY 60		
QY	61	NKQFGKATLTADKSTTAYMQLSLTSDSAVYYCAREVRLRYFDVWGQTTVTSS 118		
Db	61	NKQFGKATLTADKSTTAYMQLSLTSDSAVYYCAREVRLRYFDVWGQTTVTSS 118		

RESULT 2
US-10-700-632-7
; Sequence 7, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID LEUKEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-7

Query Match      98.4%; Score 613; DB 5; Length 118;
Best Local Similarity 98.3%; Pred. No. 8.4e-46;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60
Db 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLRYPDVWGQGTITVTS 118
Db 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLRYPDVWGQGTITVTS 118

RESULT 3
US-10-700-632-73
; Sequence 73, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73

Query Match      97.8%; Score 609; DB 5; Length 117;
Best Local Similarity 98.3%; Pred. No. 1.9e-45;
Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60
Db 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLRYPDVWGQGTITVTS 117
Db 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLRYPDVWGQGTITVTS 117

RESULT 4
US-10-366-709-39
; Sequence 39, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain CA20VH amino acid sequence
US-10-366-709-39

Query Match      85.6%; Score 533.5; DB 4; Length 120;
Best Local Similarity 84.2%; Pred. No. 7.1e-39;
Matches 101; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 2 VQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISYN 61
Db 1 VQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISYN 60

Qy 62 QKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 118
Db 61 QKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 120

RESULT 6
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
```

```
; SEQ ID NO 39
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain CA20VH amino acid sequence
US-10-366-709-39

Query Match      86.4%; Score 538.5; DB 4; Length 121;
Best Local Similarity 84.3%; Pred. No. 2.6e-39;
Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60
Db 1 QVQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 117
Db 61 NQKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 120

Qy 118 S 118
Db 121 S 121

RESULT 5
US-10-366-709-35
; Sequence 35, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain A20VH amino acid sequence
US-10-366-709-35

Query Match      85.6%; Score 533.5; DB 4; Length 120;
Best Local Similarity 84.2%; Pred. No. 7.1e-39;
Matches 101; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 2 VQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISYN 61
Db 1 VQLQQPQAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLEWGVYIPGNDISYN 60

Qy 62 QKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 118
Db 61 QKFGKATLTADKSSSTTAYMQLSSLTSEDSAVVYCAEVRLR---YFDVWGQGTITVTS 120

RESULT 6
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
```

Qy	61	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR	116
Db	188	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTY	246
Qy	117	SS 118	
Db	247	SS 248	
RESULT 8			
US-10-244-821-6			
; Sequence 6, Application US/10244821			
; Publication No. US20030143233A1			
; GENERAL INFORMATION:			
; APPLICANT: Goshorn, Stephen Charles			
; APPLICANT: Graves, Scott Stoll			
; APPLICANT: Sanderson, Joanne Elaine			
; APPLICANT: Lin, Yukang			
; APPLICANT: Sanderson, James Allen			
; APPLICANT: Reno, John M.			
; APPLICANT: Dearstynne, Erica A.			
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND			
; TITLE OF INVENTION: METHODS OF USE THEREOF			
; FILE REFERENCE: 690022.547C3			
; CURRENT APPLICATION NUMBER: US/10/244, 821			
; CURRENT FILING DATE: 2002-09-16			
; NUMBER OF SEQ ID NOS: 92			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 412			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain			
; OTHER INFORMATION: antibody-genomic streptavidin fusion			
US-10-244-821-6			
Query Match 84.3%; Score 525.5; DB 4; Length 412;			
Best Local Similarity 83.6%; Pred. No. 1.2e-37;			
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;			
Qy	1	QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPGQGLEWVGVIYPGNDISY	60
Db	128	QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGQGLEWIGAIYPGNGDTSY	187
Qy	61	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR	116
Db	188	NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWYFDVWGAGTTVTY	246
Qy	117	SS 118	
Db	247	SS 248	
RESULT 7			
US-10-150-762-6			
; Sequence 6, Application US/10150762			
; Publication No. US20030103948A1			
; GENERAL INFORMATION:			
; APPLICANT: Goshorn, Stephen C.			
; APPLICANT: Graves, Scott S.			
; APPLICANT: Schultz, Joanne E.			
; APPLICANT: Lin, Yukang			
; APPLICANT: Sanderson, James A.			
; APPLICANT: Reno, John M.			
; APPLICANT: Dearstynne, Erica A.			
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND			
; TITLE OF INVENTION: METHODS OF USE THEREOF			
; FILE REFERENCE: 690022.547C2			
; CURRENT APPLICATION NUMBER: US/10/150, 762			
; CURRENT FILING DATE: 2002-05-17			
; NUMBER OF SEQ ID NOS: 90			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 412			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain			
; OTHER INFORMATION: antibody-genomic streptavidin fusion			
US-10-150-762-6			
Query Match 84.3%; Score 525.5; DB 4; Length 412;			
Best Local Similarity 83.6%; Pred. No. 1.2e-37;			
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;			
Qy	1	QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPGQGLEWVGVIYPGNDISY	60
Db	128	QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGQGLEWIGAIYPGNGDTSY	187

```
; PRIOR APPLICATION NUMBER: 08/921,060
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/149,099
; PRIOR FILING DATE: 1993-11-03
; PRIOR APPLICATION NUMBER: 07/978,891
; PRIOR FILING DATE: 1992-11-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-238-681-11

Query Match      84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDTYS 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
;
Db 140 A 140

RESULT 10
US-10-411-037-62
; Sequence 62, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-62

Query Match      84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDTYS 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
;
Db 140 A 140

RESULT 12
US-10-410-962-62
; Sequence 62, Application US/10410962
; Publication No. US20040077836A1
```

```
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDTYS 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
;
Db 140 A 140

RESULT 11
US-10-411-026-62
; Sequence 62, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-026-62

Query Match      84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTDPGQGLEWGVYIPGNDTYS 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVMGQGTITVTS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
;
Db 140 A 140

RESULT 12
US-10-410-962-62
; Sequence 62, Application US/10410962
; Publication No. US20040077836A1
```

GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-962-62

Query Match 84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 79
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117
DB 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 139
QY 118 S 118
DB 140 A 140

RESULT 13
US-10-411-049-62
; Sequence 62, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-049-62

Query Match 84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 79
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117
DB 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 139
QY 118 S 118
DB 140 A 140

RESULT 14
US-10-327-663-14
; Sequence 14, Application US/10327663
; Publication No. US20040093621A1
; GENERAL INFORMATION:
; APPLICANT: Kenya SHITARA
; APPLICANT: Mikiko SAKURADA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Evisuke NAKANO
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
; FILE REFERENCE: 249-289
; CURRENT APPLICATION NUMBER: US/10/327,663
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: JP 2001-392753
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JP 2002-106948
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: JP 2002-319975
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-327-663-14

Query Match 84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 79
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117

```
Db      80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARSTYYGGDWYFNVMGAGTTVTVS 139
QY      118 S 118
Db      140 A 140

RESULT 15
US-10-410-930-62
; Sequence 62, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: BETA
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-930-62

Query Match      84.2%; Score 524.5; DB 4; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.1e-38;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY      1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHIKQTPOGQGLEWVGVIYPGNDDISY 60
Db      20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYNMHWKQTPOGQGLEWIGAIYPGNGDTSY 79
QY      61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 117
Db      80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARSTYYGGDWYFNVMGAGTTVTVS 139
QY      118 S 118
Db      140 A 140

Search completed: May 9, 2006, 02:04:57
Job time : 88.6277 secs
```


GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:59:22 ; Search time 14.0476 Seconds
(without alignments)
388.792 Million cell updates/sec

Title: US-10-700-632-9
Perfect score: 623
Sequence: 1 QVQLQPGAEVVKPGASVKM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	86.4	121	11	US-11-107-028-35 Sequence 35, Appl
2	524.5	84.2	140	10	US-11-183-218-62 Sequence 62, Appl
3	524.5	84.2	140	11	US-11-183-205-62 Sequence 62, Appl
4	524.5	84.2	451	11	US-11-124-620-5 Sequence 5, Appl
5	524.5	84.2	451	11	US-11-124-620-7 Sequence 7, Appl
6	524.5	84.2	451	11	US-11-208-422-25 Sequence 25, Appl
7	502	80.6	118	11	US-11-126-798-48 Sequence 48, Appl
8	502	80.6	122	10	US-11-254-182-28 Sequence 28, Appl
9	502	80.6	122	11	US-11-120-338-7 Sequence 7, Appl
10	502	80.6	122	11	US-11-106-820-7 Sequence 7, Appl
11	502	80.6	122	11	US-11-143-077-7 Sequence 7, Appl
12	502	80.6	122	11	US-11-190-364-7 Sequence 7, Appl
13	502	80.6	122	11	US-11-147-780-7 Sequence 7, Appl
14	502	80.6	122	11	US-11-143-386-7 Sequence 7, Appl
15	502	80.6	122	11	US-11-187-364-7 Sequence 7, Appl
16	502	80.6	253	11	US-11-106-820-20 Sequence 20, Appl
17	502	80.6	253	11	US-11-190-364-18 Sequence 18, Appl
18	502	80.6	253	11	US-11-147-780-18 Sequence 18, Appl
19	498	79.9	121	11	US-11-107-028-27 Sequence 27, Appl
20	494.5	79.4	121	11	US-11-107-028-37 Sequence 37, Appl
21	494	79.3	122	11	US-11-107-028-39 Sequence 39, Appl

22	492	79.0	118	9	US-10-507-662-30	Sequence 30, Appl
23	492	79.0	118	9	US-10-507-662-31	Sequence 31, Appl
24	489	78.5	118	9	US-10-507-662-36	Sequence 36, Appl
25	483.5	77.6	133	11	US-11-069-834-2	Sequence 2, Appl
26	481.5	77.3	119	11	US-11-054-689-123	Sequence 123, Appl
27	481	77.2	118	9	US-10-507-662-32	Sequence 32, Appl
28	480	77.0	124	9	US-10-932-334-13	Sequence 13, Appl
29	476.5	76.5	121	11	US-11-107-028-38	Sequence 38, Appl
30	476	76.4	118	9	US-10-507-662-33	Sequence 88, Appl
31	476	76.4	123	9	US-10-932-334-88	Sequence 33, Appl
32	476	76.4	123	9	US-10-932-334-92	Sequence 92, Appl
33	475	76.2	118	9	US-10-507-662-35	Sequence 35, Appl
34	475	76.2	118	10	US-11-297-317-2	Sequence 2, Appl
35	471	75.6	116	9	US-10-489-866-19	Sequence 19, Appl
36	471	75.6	116	9	US-10-932-334-72	Sequence 72, Appl
37	470	75.4	120	9	US-11-107-028-41	Sequence 41, Appl
38	469	75.3	120	11	US-11-226-325-198	Sequence 198, Appl
39	469	75.3	120	11	US-11-226-325-201	Sequence 201, Appl
40	469	75.3	122	9	US-10-932-334-73	Sequence 73, Appl
41	469	75.3	139	11	US-11-226-325-4	Sequence 4, Appl
42	469	75.3	139	11	US-11-097-812-31	Sequence 31, Appl
43	468.5	75.2	116	11	US-11-226-325-202	Sequence 202, Appl
44	467	75.0	120	11	US-11-226-325-202	Sequence 76, Appl
45	466.5	74.9	117	9	US-10-932-334-76	

ALIGNMENTS

RESULT 1
US-11-107-028-35
; Sequence 35, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 35
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-35

Query Match	86.4%	Score	538.5	DB	11	Length	121
Best Local Similarity	84.3%	Pred. No.	4.1e-36				
Matches	102	Conservative	7	Mismatches	9	Indels	3
Gaps	1						
QY	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHVKOTPGGLEWGVYVPGNDISY	60				
Db	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHVKOTPGGLEWGVYVPGNDISY	60				
QY	61	NKQFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLR---	YFDVWGQGTITVTS	117			
Db	61	NKQFGKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLR---	YFDVWGQGTITVTS	120			
QY	118	S	118				
Db	121	S	121				
RESULT 2							
US-11-183-218-62							
; Sequence 62, Application US/11183218							
; Publication No. US2006008906A1							


```
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (243)..(243)
; OTHER INFORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
; OTHER INFORMATION: Glutamine or Threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (244)..(244)
; OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (268)..(268)
; OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (272)..(272)
; OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (278)..(278)
; OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (301)..(301)
; OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (302)..(302)
; OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (330)..(330)
; OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (334)..(334)
; OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (336)..(336)
; OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine
; OTHER INFORMATION: or Glutamine
; US-11-124-620-5
```

```
Query Match      84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117
DB 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 120
```

```
QY 118 S 118
DB 121 A 121
```

RESULT 5

```
US-11-124-620-7
; Sequence 7, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-124-620-7
```

```
Query Match      84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117
DB 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 120

QY 118 S 118
DB 121 A 121
```

RESULT 6

```
US-11-208-423-25
; Sequence 25, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marwin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
```

```
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-25

Query Match      84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 117
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 120
QY 118 S 118
Db 121 A 121

RESULT 7
US-11-126-798-48
; Sequence 48, Application US/11/26798
; Publication No. US20060018895A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/126,798
; FILING DATE: 10-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,455
; FILING DATE: 09-May-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20003.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-25

Query Match      84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 117
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 120
QY 118 S 118
Db 121 A 121

RESULT 7
US-11-126-798-48
; Sequence 48, Application US/11/26798
; Publication No. US20060018895A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/126,798
; FILING DATE: 10-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,455
; FILING DATE: 09-May-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20003.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-126-798-48

Query Match      80.6%; Score 502; DB 11; Length 118;
Best Local Similarity 78.8%; Pred. No. 3e-33;
Matches 93; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 116
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 120

RESULT 8
US-11-254-182-28
; Sequence 28, Application US/11/254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 28
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-254-182-28

Query Match      80.6%; Score 502; DB 10; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
Db 1 QAYLQQSGAEVLRPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDIDSY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 116
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSEDSAVYYCAREVRLR---YFDVWGQGTFTVVS 120
QY 117 SS 118
Db 121 SS 122

RESULT 9
US-11-120-338-7
; Sequence 7, Application US/11/120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
```


; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof

; FILE REFERENCE: P1990R3C1

; CURRENT APPLICATION NUMBER: US/11/147,780

; PRIOR FILING DATE: 2005-06-07

; PRIOR APPLICATION NUMBER: US 60/434,115

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US 60/526,163

; PRIOR FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: PCT/US03/40426

; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 38

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-147-780-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSDSAVYFCAREVRLR-----YFDVWGQGTITVTV 116

Db 61 NQKFGKATLTVDKSSSTTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITVTV 120

Qy 117 SS 118

Db 121 SS 122

RESULT 14

US-11-143-386-7

; Sequence 7, Application US/11/143386

; Publication No. US20060051345A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS

; APPLICANT: FROHNA, PAUL A.

; FILE REFERENCE: P2134R1

; CURRENT APPLICATION NUMBER: US/11/143,386

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US 60/576,993

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-143-386-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSDSAVYFCAREVRLR-----YFDVWGQGTITVTV 116

Db 61 NQKFGKATLTVDKSSSTTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITVTV 120

Qy 117 SS 118

Db 121 SS 122

RESULT 15

US-11-187-364-7

; Sequence 7, Application US/11/187364

; Publication No. US20060062787A1

; GENERAL INFORMATION:

; APPLICANT: Hitraya, Elena

; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME

; FILE REFERENCE: P2149R1

; CURRENT APPLICATION NUMBER: US/11/187,364

; CURRENT FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/590,302

; PRIOR FILING DATE: 2004-07-22

; NUMBER OF SEQ ID NOS: 36

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-187-364-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTTPGQGLEWVGVIYPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NQKFGKATLTADKSSSTTAYMQLSSLTSDSAVYFCAREVRLR-----YFDVWGQGTITVTV 116

Db 61 NQKFGKATLTVDKSSSTTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITVTV 120

Qy 117 SS 118

Db 121 SS 122

Search completed: May 9, 2006, 02:05:57

Job time : 14.0476 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 101.749 Seconds
(without alignments)

487.964 Million cell updates/sec

Title: US-10-700-632-10

Perfect score: 586

Sequence: 1 EIVLTQSPGSLAVSPGSRVT.....CHQVLSRTTFGQTKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	586	100.0	113	8 ADO32094	Ado32094 Humanised
2	543	92.7	113	8 ADO32092	Ado32092 Mouse ant
3	543	92.7	114	8 ADO32146	Ado32146 Mouse ant
4	516	88.1	116	9 AEA38741	Aea38741 Murine an
5	516	88.1	667	9 AEA38768	Aea38768 Humanized
6	511	87.2	112	2 AAR54933	Aar54933 MAB 022 V
7	510	87.0	113	9 AAX37184	Adx37184 Murine SM
8	510	87.0	113	9 AEA88701	Aea88701 Mouse ant
9	510	87.0	133	9 ADV92466	Adv92466 Mouse SM5
10	510	87.0	133	9 ADV98529	Adv98529 Novel chi
11	510	87.0	239	9 ADV92470	Adv92470 SM5-1 chi
12	510	87.0	239	9 ADV98533	Adv98533 Novel chi
13	510	87.0	661	9 ADV92490	Adv92490 FL/Fc/chs
14	510	87.0	661	9 ADV98553	Adv98553 Novel chi
15	509	86.9	112	5 AAE23266	Aae23266 S. aureus
16	509	86.9	112	8 ADU39970	Adu39970 Antibody
17	508	86.7	112	5 AAE23264	Aae23264 S. aureus
18	507	86.5	112	5 AAE23270	Aae23270 S. aureus
19	506	86.3	113	7 ADB97820	Adb97820 HEV relat
20	505	86.2	263	2 AAW90226	Aaw90226 Anti-B7.2
21	505	86.2	268	2 AAW90222	Aaw90222 Anti-B7.2
22	505	86.2	268	2 AAW90228	Aaw90228 Anti-B7.1
23	505	86.2	273	2 AAW90224	Aaw90224 Anti-B7.1
24	505	86.2	556	2 AAW90218	Aaw90218 Bispecifi

25	505	86.2	580	2 AAW90217	Aaw90217 Bispecifi
26	503	85.8	112	5 AAE23268	Aae23268 S. aureus
27	503	85.8	244	8 ADG17481	Adg17481 Anti-CD22
28	503	85.8	244	8 ADG17486	Adg17486 Anti-CD22
29	499	85.2	113	2 AAR92215	Aar92215 LL2 Mab V
30	499	85.2	113	2 AAW27695	Aaw27695 Variable
31	499	85.2	113	7 ADC97685	Adc97685 Mouse mon
32	499	85.2	244	8 ADG17479	Adg17479 Anti-CD22
33	499	85.2	244	8 ADG17485	Adg17485 Anti-CD22
34	499	85.2	244	8 ADG17476	Adg17476 Anti-CD22
35	499	85.2	244	8 ADG17478	Adg17478 Anti-CD22
36	499	85.2	272	5 ABG31024	Abg31024 Synthetic
37	499	85.2	272	7 ADD25453	Add25453 Binding d
38	499	85.2	272	7 ADM42728	Adm42728 Synthetic
39	499	85.2	272	9 AEB95396	Aeb95396 Mouse G28
40	499	85.2	272	9 AEB94430	Aeb94430 Mouse ant
41	497	84.8	132	9 AEB08042	Aeb08042 HLA-DR sp
42	497	84.8	238	9 AEB08041	Aeb08041 Murine/hu
43	496	84.6	238	8 ADL23052	Adl23052 Mouse/hum
44	496	84.6	238	8 ADS88793	Ads88793 A mouse/h
45	496	84.6	244	8 ADG17477	Adg17477 Anti-CD22

ALIGNMENTS

RESULT 1

ADO32094

ID ADO32094 standard; protein; 113 AA.

XX AC ADO32094;

XX AC ADO32094;

DT 12-AUG-2004 (first entry)

DE Humanised mouse anti-CD33 antibody My9-6 light chain SEQ ID NO:10.

XX anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;

KW My9-6; light chain.

XX Mus musculus.

OS Homo sapiens.

OS Synthetic.

XX WO2004043344-A2.

PN WO2004043344-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WFI; 2004-411619/38.

XX New antibodies that bind to CD33, useful for treating a disease

PT associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.

PS Claim 14; SEQ ID NO 10; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its

CC epitope-binding fragment comprising: (a) at least one complementarity-

CC determining region (CDR); or (b) at least heavy chain variable region

CC comprising 3 CDRs, and at least one light chain variable region, where

CC the CDR has the ability to bind CD33. Also described: (1) an

CC immunconjugate comprising the antibody or its epitope-binding fragment

CC linked to a drug or prodrug; (2) a composition comprising the antibody or

CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 light
 CC chain variable region, which is used in an example from the present
 CC invention.

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 586; DB 8; Length 113;
 Best Local Similarity 100.0%; Pred. No. 3.3e-38;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTR 60

DB 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTR 60

QY 61 ESGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

DB 61 ESGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

RESULT 2

AD032092
 ID AD032092 standard; protein; 113 AA.

XX AC

AD032092;

XX DT 12-AUG-2004 (first entry)

XX DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.

XX KW anti-CD33 antibody; epitope-binding fragment;
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;
 KW light chain.

XX OS Mus musculus.

XX PN WO2004043344-A2.

XX PD 27-MAY-2004.

XX PF 05-NOV-2003; 2003WO-US032737.

XX PR 07-NOV-2002; 2002US-0424332P.

XX PA (IMMU-) IMMUNOGEN INC.

XX PI Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

DR N-PSDB; ADO321139.

XX PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.

XX PS Claim 8; SEQ ID NO 8; 124pp; English.

XX CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain
 CC variable region, which is used in an example from the present invention.

XX SQ Sequence 113 AA;

Query Match 92.7%; Score 543; DB 8; Length 113;

Best Local Similarity 93.8%; Pred. No. 7.4e-35;

Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTRE 61

DB 2 IVLTQSPGSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIIPGQSPKLLIIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

DB 62 SGVPRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGQTKLEIKR 113

RESULT 3

AD032146

ID AD032146 standard; protein; 114 AA.

XX AC

AD032146;

XX DT 12-AUG-2004 (first entry)

XX DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.

XX KW anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunoconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.

XX OS Mus musculus.

PN WO2004043344-A2.
 XX 27-MAY-2004.
 XX
 XX
 XX 05-NOV-2003; 2003WO-US032737.
 XX
 XX 07-NOV-2002; 2002US-0424332P.
 XX (IMMU-) IMMUNOGEN INC.
 XX
 PI Hoffee MG, Tavares D, Lutz RJ;
 XX WPI; 2004-411619/38.
 XX
 XX New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 XX
 XX Example 3; SEQ ID NO 62; 124pp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarity-
 CC determining region (CDR); or (b) at least one heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunoconjugate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunoconjugate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunoconjugate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody light chain homologous
 CC amino acid sequence, which is used in an example from the present
 CC invention.
 XX
 XX Sequence 114 AA;
 Query Match 92.7%; Score 543; DB 8; Length 114;
 Best Local Similarity 93.8%; Pred. No. 7.4e-35;
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IVLTSQPSGLAVSPGERTVMTCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
 DB 2 IMLTQSPSSLAVSNGEKVTMTCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
 QY 62 SGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113
 DB 62 SGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113
 RESULT 4
 AEA38741
 ID AEA38741 standard; protein; 116 AA.
 XX

AC AEA38741;
 XX 11-AUG-2005 (first entry)
 XX
 XX Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.
 DE
 XX Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;
 KW cancer cell proliferation inhibitor;
 KW transforming growth factor-beta-antagonist; light chain variable region.
 XX
 XX Mus musculus.
 XX
 XX Key Location/Qualifiers
 FT Region 24..40
 FT /note= "Complementarity determining region (CDR) - L1"
 FT Region 56..62
 FT /note= "Complementarity determining region (CDR) - L2"
 FT Region 95..102
 FT /note= "Complementarity determining region (CDR) - L3"
 XX
 XX WO2005050200-A2.
 XX
 XX 02-JUN-2005.
 XX
 XX 04-NOV-2004; 2004WO-US036651.
 XX
 XX 13-NOV-2003; 2003US-0520398P.
 XX 31-MAR-2004; 2004US-0557951P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Filvaroff EH;
 XX
 XX WPI; 2005-417772/42.
 XX
 XX Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.
 XX
 XX Example 2; SEQ ID NO 1; 109pp; English.
 XX
 CC The present invention relates to the screening of candidate molecules
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is murine anti-TGF-beta antibody
 CC (2G7) variable light chain (VL) monoclonal antibody protein.
 XX
 XX Sequence 116 AA;
 Query Match 88.1%; Score 516; DB 9; Length 116;
 Best Local Similarity 86.7%; Pred. No. 9.5e-33;
 Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGSLAVSPGERTVMTCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTR 60
 DB 1 DIMTQSPSSLAVSNGEKVTMTCKSSQSVLYISNQNLYLAWYQIQGSPKLLIYWASTR 60
 QY 61 ESGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113

Db 61 ESGVDPRTGSGDFTLTSSVQAEADLAVYCHQYLSSDTFGGKTLEIKR 113
 |||||
 RESULT 5
 AEA38768
 ID AEA38768 standard; protein; 667 AA.
 XX AEA38768;
 XX 11-AUG-2005 (first entry)
 XX Humanized murine anti-TGF-beta antibody protein, chimL.chimH, SEQ: 28.
 XX Monoclonal antibody; animal disease model; metastasis; cytostatic;
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;
 KW cancer cell proliferation inhibitor;
 KW transforming growth factor-beta-antagonist; humanized antibody;
 KW chimeric antibody.
 XX Mus musculus.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH Misc-difference 220
 FT /label= Unknown
 FT
 XX WO2005050200-A2.
 XX
 XX 02-JUN-2005.
 XX
 XX 04-NOV-2004; 2004WO-US036651.
 XX
 XX 13-NOV-2003; 2003US-0520398P.
 PR 31-MAR-2004; 2004US-0557951P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Filvaroff EH;
 XX
 XX WPI; 2005-417772/42.
 XX
 XX Screening compounds useful for treating tumor metastasis involves
 PT administering a test compound to non-human animal model bearing soft
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue
 PT growth/bone metastasis.
 XX
 XX Example 2; SEQ ID NO 28; 109pp; English.
 XX
 XX The present invention relates to the screening of candidate molecules
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment
 CC of tumor metastasis and treatment methods using such molecules. The
 CC screening method of the invention involves administering several test
 CC substances to a non-human syngeneic immunocompetent animal model bearing
 CC at least one soft tissue or bone metastasis optionally in presence of a
 CC primary tumor, determining the effects of these test substances on the
 CC soft tissue or bone metastasis and growth of the primary tumor and
 CC identifying a test substance inhibiting soft tissue growth or bone
 CC metastasis without adverse effect on the status of the primary tumor. The
 CC invention is useful in the diagnosis and treatment of breast cancer,
 CC colorectal cancer, liver and lung metastases, bone destruction and bone
 CC loss. The animal models of the present invention is useful to screen
 CC substances useful for the prophylaxis or treatment of soft tissue and/or
 CC bone metastases which may additionally be effective in treating the
 CC primary tumor. The present sequence is humanized murine anti-transforming
 CC growth factor-beta (anti-TGF-beta) antibody (also referred as humanized
 CC monoclonal antibody 267) chimeric protein.
 XX
 XX Sequence 667 AA;

Query Match 88.1%; Score 516; DB 9; Length 667;
 Best Local Similarity 86.7%; Pred. No. 4.6e-32;
 Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGSLAVSPGERVTMTCKSSQSVFFSSQKYNLAYWQIQPGSPRLIIYWASTR 60
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 DIMTQSPSSLAVSAGEKVTMTCKSSQSVLYSSNQKNLAYWQKPGQSPKLLIYWASTR 60
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 ESGVDPDRFTGSGDFTLTITSSVQAEADLAVYCHQYLSSDTFGGKTLEIKR 113
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ESGVDPDRFTGSGDFTLTITSSVQAEADLAVYCHQYLSSDTFGGKTLEIKR 113
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 6
 AAR54933
 ID AAR54933 standard; peptide; 112 AA.
 XX AAR54933;
 XX AC AAR54933;
 XX 25-MAR-2003 (revised)
 DT 19-OCT-1994 (first entry)
 XX MAB 022 VK chain.
 DE
 XX Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
 KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;
 KW CDR; complementarity determining region; VH; heavy chain variable region;
 KW VK; kappa chain variable region; mononuclear phagocyte; PCR;
 KW polymerase chain reaction; primer; site-directed mutagenesis;
 KW monoclonal antibody; MAB.
 XX
 XX Mus sp.
 OS
 XX WO9410332-A1.
 FN
 XX 11-MAY-1994.
 PD
 XX 04-NOV-1993; 93WO-US010384.
 PF
 XX 04-NOV-1992; 92GB-00023377.
 PR
 XX (MEDA-) MEDAREX INC.
 PA
 XX Tempest PR, Harris WJ, Carr FJ;
 PI
 XX WPI; 1994-167486/20.
 DR
 XX New humanised antibodies to Fc receptors - used for diagnosis or for
 PT treatment of e.g. cancer, allergies and infectious and auto-immune
 PT diseases.
 PT
 XX Disclosure; Page 23; 36pp; English.
 PS
 XX Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
 CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-
 CC 1), VH chains from human IgG NEMW or KOL, and VK chains from Ig REI.
 CC Sequences are provided for mouse 022 VH (AAR54931), humanized NEMW-based
 CC VH (022 NMVH, AAR54929), humanized KOL-based VH (022 KLVH, AAR54930),
 CC mouse 022 VK (AAR54933) and humanized REI-based VK (022 HUVK, AAR54932).
 CC During hAb production, VH and VK cDNAs were PCR amplified using primers
 CC given in AAQ065378-87. Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was
 CC performed using oligos AAQ05388-89. The hAbs can be used in
 CC heteroantibody, bifunctional antibody and immunotoxin production.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 112 AA;
 SQ
 Query Match 87.2%; Score 511; DB 2; Length 112;
 Best Local Similarity 88.3%; Pred. No. 2.2e-32;
 Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 2 IIVLTQSPGSLAVSPGERVTMTCKSSQSVFFSSQKYNLAYWQIQPGSPRLIIYWASTRE 61
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||


```

DT 10-MAR-2005 (first entry)
XX
DE Mouse SM5-1 (mSM5-1) light chain variable region protein.
XX
KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note="Signal peptide"
FT Region 21..133
FT /note="light chain variable region gene (VL)"
FT Protein 21..133
FT /note="Mature Mouse SM5-1 (mSM5-1) light chain variable
FT region protein"
XX
XX US2004254108-A1.
XX
XX 16-DEC-2004.
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
XX 25-NOV-2003; 2003CN-01119930.
XX (MAJU/) MA J.
XX PA (GUOY/) GUO Y.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-030218/03.
XX N-PSDB; ADV92465.
XX
XX New chimeric protein comprises an Flt3 ligand and a proteinous or
XX peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
XX e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
XX Example 3; SEQ ID NO 10; 158pp; English.
XX
XX The present invention relates to a chimeric protein having a Flt3 ligand
XX (FL) or its biologically active fragment and a proteinous or peptidyl
XX tumoricidal agent. The invention is useful for treating malignancy,
XX neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
XX vaccine for eliciting an immune response. The invention is also useful in
XX gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light
XX chain variable region protein.
XX
SQ Sequence 133 AA;
Query Match 87.0%; Score 510; DB 9; Length 133;
Best Local Similarity 86.6%; Pred. No. 3.1e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTSQPSGLAVSPGERTVMSCKSSQSVFSSQKNYLAWYQQIPQSPRLIYWASTRE 61
Db 22 IMWTQSPSLAVSAGEKVTMSCKSSQSVLYSSNKNYLAWYQQKPGQSPKLLIYWASTRE 81
QY 62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQGTKEIKR 113
Db 82 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQGTKEIKR 133
RESULT 10
ADV98529
ID ADV98529 standard; protein; 133 AA.
XX
AC ADV98529;
XX
XX 24-MAR-2005 (first entry)
XX

```

```

DE Novel chimeric protein-related mSM5-1 light chain protein SeqID10.
XX
KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
OS Mus sp.
XX
XX WO2005001048-A2.
XX
XX 06-JAN-2005.
XX
XX 04-JUN-2004; 2004WO-US017765.
XX
XX 13-JUN-2003; 2003CN-00129290.
XX 25-NOV-2003; 2003CN-01119930.
XX 26-NOV-2003; 2003US-00723003.
XX 28-NOV-2003; 2003TW-00133577.
XX
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-075540/08.
XX N-PSDB; ADV98528.
XX
XX New chimeric protein for preventing or treating neoplastic conditions,
XX e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
XX Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
XX agent.
XX
XX Example 3; SEQ ID NO 10; 147pp; English.
XX
XX This invention relates to a novel chimeric protein comprising an Flt3
XX ligand, or its biological fragment, and a proteinous or peptidyl
XX tumoricidal agent. The invention may be useful for the production of
XX compounds with a cytostatic activity or a vaccine. The composition and
XX methods are useful for preventing or treating neoplastic conditions, such
XX as melanoma, breast cancer or hepatocellular carcinoma. The present
XX sequence is that of a protein which is related to the chimeric proteins
XX of the invention.
XX
SQ Sequence 133 AA;
Query Match 87.0%; Score 510; DB 9; Length 133;
Best Local Similarity 86.6%; Pred. No. 3.1e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTSQPSGLAVSPGERTVMSCKSSQSVFSSQKNYLAWYQQIPQSPRLIYWASTRE 61
Db 22 IMWTQSPSLAVSAGEKVTMSCKSSQSVLYSSNKNYLAWYQQKPGQSPKLLIYWASTRE 81
QY 62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQGTKEIKR 113
Db 82 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQGTKEIKR 133
RESULT 11
ADV92470
ID ADV92470 standard; protein; 239 AA.
XX
AC ADV92470;
XX
XX 10-MAR-2005 (first entry)
XX
XX SM5-1 chimeric antibody (ChSM) light chain protein.
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Homo sapiens.
XX Mus sp.
XX Chimeric.

```

```

XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT Protein /label= Signal peptide
XX FT Protein 21..239
XX FT Protein /note= "Mature SM5-1 chimeric antibody (ChSM) light chain protein"
XX FT Region 21..133
XX FT Region /note= "Light chain variable region gene (VL)"
XX FT Region 134..239
XX FT Region /note= "Human kappa chain constant cDNA (CL)"
XX FN US2004254108-A1.
XX PD 16-DEC-2004.
XX PP 26-NOV-2003; 2003US-00723003.
XX PR 13-JUN-2003; 2003CN-00129290.
XX PR 25-NOV-2003; 2003CN-01119930.
XX PA (MAJJ/) MA J.
XX PA (GUOY/) GUO Y.
XX PI Ma J, Guo Y;
XX PS WPI; 2005-030218/03.
XX PS N-PSDB; ADV92469.
XX PT New chimeric protein comprises an Flt3 ligand and a proteinous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX PS Example 3; SEQ ID NO 14; 158pp; English.
XX CC The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma, and as a CC vaccine for eliciting an immune response. The invention is also useful in CC gene therapy. The present sequence is the SM5-1 chimeric antibody (ChSM) CC light chain protein.
XX SQ Sequence 239 AA;
Query Match 87.0%; Score 510; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 5.3e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 2 IVLTQSPGSLAVSPGKRVMTSCSKSSQSVFSSQKYNLAWYQIQPGSPRLIIYWASTRE 61
Db 22 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKYNLAWYQKPGSPKLLIYWASTRE 81
Qy 62 SGVPDRFTGSGGDTFTLTISVQPEDLAIYCHQYLSRFTFGGKLEIKR 113
Db 82 SGVPDRFTGSGGDTFTLTISVQAEADLAVYCHQYFSSYTFGGGKLEIKR 133
RESULT 12
ADV98533
ID ADV98533 standard; protein; 239 AA.
XX AC ADV98533;
XX DT 24-MAR-2005 (first entry)
XX DE Novel chimeric protein-related ChSM light chain protein SeqID14.
XX KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
XX KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX OS Mus sp.
XX OS Synthetic.

```

```

XX WO2005001048-A2.
XX PD 06-JAN-2005.
XX PF 04-JUN-2004; 2004WO-US017765.
XX PR 13-JUN-2003; 2003CN-00129290.
XX PR 25-NOV-2003; 2003CN-01119930.
XX PR 26-NOV-2003; 2003US-00723003.
XX PR 28-NOV-2003; 2003TW-00133577.
XX PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX PI Ma J, Guo Y;
XX PS WPI; 2005-075540/08.
XX PS N-PSDB; ADV98532.
XX PT New chimeric protein for preventing or treating neoplastic conditions, PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal agent.
XX PS Example 3; Fig 9; 147pp; English.
XX CC This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinous or peptidyl tumoricidal agent. The invention may be useful for the production of CC compounds with a cytostatic activity or a vaccine. The composition and CC methods are useful for preventing or treating neoplastic conditions, such as melanoma, breast cancer or hepatocellular carcinoma. The present CC sequence is that of a protein which is related to the chimeric proteins of the invention. Note: Two sequences were allocated this SeqID number in CC the specification, the alternative sequence is shown on page 21.
XX SQ Sequence 239 AA;
Query Match 87.0%; Score 510; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 5.3e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 2 IVLTQSPGSLAVSPGKRVMTSCSKSSQSVFSSQKYNLAWYQIQPGSPRLIIYWASTRE 61
Db 22 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKYNLAWYQKPGSPKLLIYWASTRE 81
Qy 62 SGVPDRFTGSGGDTFTLTISVQPEDLAIYCHQYLSRFTFGGKLEIKR 113
Db 82 SGVPDRFTGSGGDTFTLTISVQAEADLAVYCHQYFSSYTFGGGKLEIKR 133
RESULT 13
ADV92490
ID ADV92490 standard; protein; 661 AA.
XX AC ADV92490;
XX DT 10-MAR-2005 (first entry)
XX DE FL/Pc/chSMFv fusion protein.
XX KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
XX KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
XX KW breast cancer; hepatocellular carcinoma.
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Chimeric.
XX PH Key Location/Qualifiers
XX FT Peptide 1..26
XX FT Protein /label= Signal peptide
XX FT Protein 27..661

```

```

FT Region /note= "Mature FL/Fc/chSMFv fusion protein"
FT 27..182
FT /note= "Flt3 ligand extracellular region (FLex)"
FT 183..197
FT /note= "Hinge region"
FT 198..307
FT /note= "CH2 region"
FT Misc-difference 271
FT /note= "Encoded by TGC"
FT Region 308..414
FT /note= "CH3 region"
FT Region 415..533
FT /note= "Heavy chain variable region gene (VH)"
FT Region 534..556
FT /note= "Linker region"
FT Region 557..661
FT /note= "Light chain variable region gene (VL)"
FT
XX
PN US2004254108-A1.
XX
XX 16-DEC-2004.
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
XX 25-NOV-2003; 2003CN-01119930.
XX
XX (MAJJ/) MA J.
XX (GUOY/) GUO Y.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-030218/03.
XX N-PSDB; ADV92489.
XX
XX New chimeric protein comprises an Flt3 ligand and a proteinous or
XX peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
XX e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
XX Claim 23; SEQ ID NO 34; 158pp; English.
XX
XX The present invention relates to a chimeric protein having a Flt3 ligand
XX (FL) or its biologically active fragment and a proteinous or peptidyl
XX tumoricidal agent. The invention is useful for treating malignancy,
XX neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma, and as a
XX vaccine for eliciting an immune response. The invention is also useful in
XX gene therapy. The present sequence is the FL/Fc/chSMFv fusion protein.
XX
XX Sequence 661 AA;
SQ
Query Match 87.0%; Score 510; DB 9; Length 661;
Best Local Similarity 86.6%; Pred. NO. 1.3e-31;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTQSPGSLAVSPGKRVMTCSKSSQSVFSSQKNYLAWYQQIPGQSPRLIYWASTRE 61
DB 550 IMWTQSPSSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 609
QY 62 SGVPRDFTGSGSGTDFTLTISSVQPEDLAIIYVCHQYLSRTRFGQGTKEIKR 113
DB 610 SGVPRDFTGSGSGTDFTLTISSVQAEADLAVYVCHQYVFSSTYFGGTKEIKR 661
RESULT 14
ADV98553
ID ADV98553 standard; protein; 661 AA.
XX
XX ADV98553;
AC
XX 24-MAR-2005 (first entry)
DT
XX Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34.
DE
XX

```

```

KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
XX Homo sapiens.
OS
OS Mus sp.
OS Synthetic.
XX
XX WO2005001048-A2.
XX
XX 06-JAN-2005.
XX
XX 04-JUN-2004; 2004WO-US017765.
XX
XX 13-JUN-2003; 2003CN-00129290.
XX 25-NOV-2003; 2003CN-01119930.
XX 26-NOV-2003; 2003US-00723003.
XX 28-NOV-2003; 2003TW-00133577.
XX
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-075540/08.
XX N-PSDB; ADV98552.
XX
XX New chimeric protein for preventing or treating neoplastic conditions,
XX e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
XX Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
XX agent.
XX
XX Claim 23; SEQ ID NO 34; 147pp; English.
XX
XX This invention relates to a novel chimeric protein comprising an Flt3
XX ligand, or its biological fragment, and a proteinous or peptidyl
XX tumoricidal agent. The invention may be useful for the production of
XX compounds with a cytostatic activity or a vaccine. The composition and
XX methods are useful for preventing or treating neoplastic conditions, such
XX as melanoma, breast cancer or hepatocellular carcinoma. The present
XX sequence is that of a protein which is related to the chimeric proteins
XX of the invention.
XX
XX Sequence 661 AA;
SQ
Query Match 87.0%; Score 510; DB 9; Length 661;
Best Local Similarity 86.6%; Pred. NO. 1.3e-31;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTQSPGSLAVSPGKRVMTCSKSSQSVFSSQKNYLAWYQQIPGQSPRLIYWASTRE 61
DB 550 IMWTQSPSSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 609
QY 62 SGVPRDFTGSGSGTDFTLTISSVQPEDLAIIYVCHQYLSRTRFGQGTKEIKR 113
DB 610 SGVPRDFTGSGSGTDFTLTISSVQAEADLAVYVCHQYVFSSTYFGGTKEIKR 661
RESULT 15
AAE29266
ID AAE29266 standard; protein; 112 AA.
XX
XX AAE29266;
AC
XX 27-JAN-2003 (first entry)
DT
XX
XX S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.
DE
XX
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH

```

FT Region 24. .40
FT /note= "CDR1"
FT 56. .62
FT /note= "CDR2"
FT 95. .102
FT /note= "CDR3"
XX
FN WO200272600-A2.
XX
XX
XX 19-SEP-2002.
XX
XX 28-JAN-2002; 2002WO-US002296.
XX
XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
XX (INHI-) INHIBITEX INC.
XX
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759834/82.
DR N-PSDB; AAD46865.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
XX Claim 11; Page 35; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VLA-1 (variable light sequence) protein
XX
XX Sequence 112 AA;
SQ

Query Match 86.9%; Score 509; DB 5; Length 112;
Best Local Similarity 87.4%; Pred. No. 3.2e-32;
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IVLTQSPGSLAVSPGERVTWCKSSQSVFFSSQKKNYLAWYQQIIPGQSPRLIIYWASTRE 61
Db 2 IMVTQSPSSSLAVSAGEKVTWCKSSQSVLYSSNKNYLAWYQQKPGQSPKLLIYWASTRE 61

Qy 62 SGVPDRFTGSGGTDFTLTITSSVQPEDLAIYYCHQYLSRRTFGQGTKLEIK 112
Db 62 SGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCHQYLSRRTFGQGTKLEIK 112

Search completed: May 9, 2006, 01:25:26
Job time : 103.749 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.1212 Seconds
(without alignments)
635.031 Million cell updates/sec

Title: US-10-700-632-10
Perfect score: 586
Sequence: 1 EIVLTQSPGSLAVSPGSRVT.....CHQYLSRTRFGQGTKLEIKR 113
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	83.6	111	2 G30502	Ig kappa chain V r
2	478	81.6	112	2 S41393	Ig kappa chain V r
3	477	81.4	118	2 P70356	Ig kappa chain V r
4	473	80.7	138	2 S26040	Ig kappa chain pre
5	471	80.4	103	2 PH1054	Ig kappa chain V r
6	469.5	80.1	113	2 S34002	Ig kappa chain V r
7	467	79.7	112	2 S09970	Ig kappa chain V-J
8	467	79.7	112	2 S43103	Ig kappa chain V-J
9	467	79.7	133	2 P50023	Ig kappa chain pre
10	465.5	79.4	114	1 K4HULN	Ig kappa chain V-I
11	463.5	79.1	145	2 PL0014	Ig kappa chain pre
12	462	78.8	112	2 PL0265	Ig kappa chain V r
13	461.5	78.8	120	2 S51147	antibody light cha
14	461.5	78.8	240	2 S06084	Ig kappa chain pre
15	460	78.5	113	2 P70407	Ig light chain V r
16	460	78.5	133	1 K4HUUI	Ig kappa chain pre
17	459	78.3	101	2 S26337	Ig kappa chain pre
18	457.5	78.1	134	2 S49531	anti-Sm antibody V
19	455.5	77.7	134	2 PC1214	Ig kappa chain pre
20	451	77.0	138	2 A53261	Ig kappa chain pre
21	447.5	76.4	113	2 S30520	Ig kappa chain V r
22	447.5	76.4	113	2 S34003	Ig kappa chain V r
23	447.5	76.4	220	2 A31790	Ig kappa chain V r
24	444.5	75.9	113	2 A49260	antitumor monoclon
25	444.5	75.9	134	1 K4HU17	Ig kappa chain pre
26	443.5	75.7	133	2 PL0263	Ig kappa chain V r
27	443.5	75.7	132	2 S46373	Ig kappa chain V-J
28	442.5	75.5	113	2 JC2270	PL7-6 antibody lig
29	442	75.4	113	2 PT0408	Ig light chain V r

30	441.5	75.3	113	2 S30523	Ig kappa chain V r
31	436.5	74.5	135	2 S38807	Ig light chain V-J
32	436.5	74.5	214	2 S68212	Ig kappa chain (Ma
33	436	74.4	104	2 PH1102	Ig light chain V r
34	435	74.2	104	2 PH1101	Ig light chain V r
35	433.5	74.0	112	2 F30538	Ig kappa chain V r
36	433.5	74.0	129	2 S40347	Ig kappa chain - h
37	432.5	73.8	112	2 S30538	Ig kappa chain V r
38	432.5	73.8	114	2 S44116	Ig kappa chain V-J
39	432	73.7	104	2 PH1104	Ig light chain V r
40	431.5	73.6	114	2 S44119	Ig kappa chain V-J
41	430	73.4	103	2 PH1050	Ig light chain V r
42	430	73.4	109	2 G30601	Ig kappa chain V-I
43	429	73.2	104	2 PH1103	Ig light chain V r
44	428	73.0	129	2 S49532	anti-Sm antibody V
45	427.5	73.0	113	2 PL0264	Ig kappa chain V r

ALIGNMENTS

RESULT 1

G30502
Ig kappa chain V region (A52) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: G30502
R:Elilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m
A:Reference number: A30502; MUID:98315787; PMID:2457627
A:Accession: G30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <EIL>
A:Cross-references: UNIPARC:UPI0000176AF0
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 490; DB 2; Length 111;
Best Local Similarity 84.5%; Pred. No. 7.5e-35;
Matches 93; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy	2	IVLTQSPGSLAVSPGSRVTMSCKSSQSVLPFSSQKYNLAWYQQIPGSPRLIIYWASTRE	61
Db	2	IMVTQSPSSSLAVAGEKVTMSCKSSQSVLPFSSQKYNLAWYQQKPGSPKLLIYWASTRE	61
Qy	62	SGVPDRFTGSGSGDFTLTITSSVQPEDLAIIYCHQYLSRTRFGQGTKLEI	111
Db	62	SGVPDRFTGSGSGDFTLTITSSVQAEADLAVIYCHQHFSSWTFGGTTKLEI	111

RESULT 2

S41393
Ig kappa chain V region (12.5H VL) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S41393
R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
C:Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IgM anti-I-
A:Reference number: S41393
A:Accession: S41393
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <MAR>
A:Cross-references: UNIPARC:UPI0000176CCB; EMBL:Z29536
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 478; DB 2; Length 112;

F;41-121/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 473; DB 2; Length 138;
Best Local Similarity 77.9%; Pred.No.2.5e-33;
Matches 88; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVPFSSQKNYLAWYQQIPGOSPRLLIYWASTR 60
:|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 26 DIVMSQSPSLSLTVSGEKVTMNCKSSQLSYNNQKNYLAWYQOKPGSQPKLIYWASTR 85
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 ESGVDRFTGSGSGTDFTLTISVVQPEDLAIIYCHYLVSSRTTGGQGKLIKRR 113
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 86 ESGVDRFTGSGSGTDFTLTISVKAEDLAVYFCQQYYSLTFAGTKLEKR 138
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
PH1054
IG light chain V region (clone 202.135) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1054
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IgG anti-DNA antibodies are the products of clonally selected B cells
A;Reference number: PH0971; PMID:92381444; PMID:1512540
A;Accession: PH1054
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TL>
A;Cross-references: UNIPARC:UPI0000176AAE
A;Experimental source: B cell, strain [MZB x NZW]Fl
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 471; DB 2; Length 103;
Best Local Similarity 87.3%; Pred.No.2.8e-33;
Matches 89; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMSCKSSQSVPFSSQKNYLAWYQQIPGOSPRLLIYWASTRE 61
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 2 IMVTQSPSSLAVSAGEKVMTSCSKSSQSVLYSSNQKNYLAWYQOKPGSQPKLIYWASTRE 61
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 62 SGVDPDRFTGSGSGTDFTLTISVVQPEDLAIIYCHYLVSSRTFF 103
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 62 SGVDPDRFTGSGSGTDFTLTISVQAEDLAVVYCHYLVSSVTF 103
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
S34002
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34002; S30522
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal antibody heavy chain genes
A;Reference number: S34001; PMID:93209281; PMID:7681398
A;Accession: S34002
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <VAR>
A;Cross-references: UNIPARC:UPI0000176D32; EMBL:Z18328
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 469.5; DB 2; Length 113;
Best Local Similarity 78.8%; Pred.No.4.1e-33;
Matches 89; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVPFSSQKNYLAWYQQIPGOSPRLLIYWASTR 60
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 1 DIVMTQSPDLSVSLGERATINCKSSQSVLYSSNNKNYLAHYQKPGQPPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 112
Db 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 113
RESULT 7
S09970
Ig kappa chain V-J region (4C8) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C/Accession: S09970
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A/Reference number: S09955; MUID:90269328; PMID:2347362
A/Accession: S09970
A/Molecule type: mRNA
A/Residues: 1-112 <REI>
A/Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:G55406; PIDN:CAA36151.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
Query Match 79.7%; Score 467; DB 2; Length 112;
Best Local Similarity 77.7%; Pred. No. 6.7e-33;
Matches 87; Conservative 14; Mismatches 11; Indels 0; Gaps 0;
QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQGSPRLLIYWASTR 60
Db 1 DIVMSQSPSLTSGVGEKVTMCKSSQSVLLYSNNKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 112
Db 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 112
RESULT 8
S43103
Ig kappa chain V-J region (4B1 VL) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
C/Accession: S43103
R;Gilbert, D.; Brard, F.; Margartte, C.; Delpach, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A/Description: An idotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A/Reference number: S42484
A/Accession: S43103
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-112 <GL>
A/Cross-references: UNIPARC:UPI0000116626; EMBL:Z31353; NID:G467574; PIDN:CAA83231.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
Query Match 79.7%; Score 467; DB 2; Length 112;
Best Local Similarity 80.4%; Pred. No. 6.7e-33;
Matches 90; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQGSPRLLIYWASTR 60
Db 1 DIVMSQSPSLAVSAGEKVTMCKSSQSVLLYSNNKNYLAHYQKPGQSPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 112
Db 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIK 112
RESULT 9
PS0023
Ig kappa chain precursor V region (6A4) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C/Accession: PS0023
R;Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A/Reference number: PS0023; MUID:89232725; PMID:3149944
A/Accession: PS0023
A/Molecule type: mRNA
A/Residues: 1-133 <MAR>
A/Cross-references: UNIPARC:UPI0000176787
A/Experimental source: strain BALB/c
A/Note: the amino-terminal four residues of the mature protein were directly sequenced
C/Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>
F;36-116/Domain: immunoglobulin homology <IMM>
Query Match 79.7%; Score 467; DB 2; Length 133;
Best Local Similarity 79.6%; Pred. No. 7.9e-33;
Matches 90; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQGSPRLLIYWASTR 60
Db 21 DIVMSQSPSLAVSAGEKVTMCKSSQSVLLYSNNKNYLAHYQKPGQSPKLLIYWASTR 80
QY 61 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIKR 113
Db 81 ESGVDPDRFTGSGGTDFLTLSVQPEDLAHYCHQYLS-SRTFGQGTKEIKR 133
RESULT 10
K4HULN
Ig kappa chain V-IV region (Len) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C/Accession: A01903; F61458
R;Schneider, M.; Hilechmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A/Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV
A/Reference number: A01903; MUID:76004342; PMID:50995
A/Accession: A01903
A/Molecule type: protein
A/Residues: 1-114 <SCH>
A/Cross-references: UNIPARC:UPI0000173708
A/Note: this is the first completely sequenced V region of a new kappa chain subgroup,
A/Note: the C region of this chain has the Inv (3) marker
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A/Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass
A/Reference number: A61458; MUID:90039128; PMID:2478651
A/Accession: F61458
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <BRO>
A/Cross-references: UNIPARC:UPI0000173709
C/Comment: This is a Bence Jones protein.
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
F;23-94/Disulfide bonds: #status predicted
Query Match 79.4%; Score 465.5; DB 1; Length 114;
Best Local Similarity 78.1%; Pred. No. 9.1e-33;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQGSPRLLIYWASTR 60
Db 1 DIVMTQSPNSLAVSLGERATINCKSSQSVLYSSNNKNYLAHYQKPGQPPKLLIYWASTR 60

Wed May 10 09:27:23 2006

```
RESULT 15
PT0407
Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PT0407
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodies
A:Reference number: PT0376; MUID:91147903; PMID:1900082
A:Accession: PT0407
A:Molecule type: DNA
A:Residues: 1-113 <BEH>
A:Cross-references: UNIPARC:UPI0000176A05
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match          78.5%; Score 460; DB 2; Length 113;
Best Local Similarity 78.8%; Pred. No. 2.6e-32;
Matches 89; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGSLAVSPGERVTMCSKSSQSVFFSSQKNYLAWYQQIPGQSPRLIIYWASTR 60
   :|::||| ||||| :|::||| ||||| :|::||| ||||| :|::||| |||||
Db 1 DIVISQSPSSLAVSAGEKVTMCSKSSQSLLSRTRKNYLAWYQQKPGQSPKLLIYWASTR 60
   :|::||| ||||| :|::||| ||||| :|::||| ||||| :|::||| |||||

Qy 61 ESGVPRDRTGSGSGTDFLTITSSVQPEDLAIIYCHQYLSSRTFGGQTKLEIKR 113
   | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ECGVPRDRTGSGSGTDFLTITSSVQAEGLAVIYCKQSYNLVTFGGGQTKLEIKR 113
   | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: May 9, 2006, 01:33:50
Job time : 18.1212 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:41 ; Search time 103.461 Seconds
(without alignments)
770.577 Million cell updates/sec

Title: US-10-700-632-10

Perfect score: 586

Sequence: 1 E1VLTPGSLAVSPGRVT.....CHQVLSRTFTGQTKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464.5	79.3	114	1 KV4A HUMAN	P01625 homo sapien
2	460	78.5	133	1 KV4B HUMAN	P06313 homo sapien
3	457.5	78.1	134	1 KV4C HUMAN	P06314 homo sapien
4	452.5	77.2	240	2 Q52L64 MOUSE	Q52L64 mus musculus
5	433.5	74.0	255	2 Q6KB05 MOUSE	Q6KB05 mus musculus
6	425	72.5	129	1 KV3L HUMAN	P18135 homo sapien
7	420	71.7	121	1 KV40 HUMAN	P06312 homo sapien
8	417	71.2	109	1 KV3E HUMAN	P01623 homo sapien
9	415	70.8	109	1 KV3B HUMAN	P01620 homo sapien
10	414	70.6	129	1 KV3M HUMAN	P18136 homo sapien
11	413	70.5	109	1 KV3D HUMAN	P01622 homo sapien
12	412	70.3	109	2 Q9UL78 HUMAN	Q9UL78 homo sapien
13	406.5	69.4	109	1 KV4D HUMAN	P83593 homo sapien
14	406.5	69.4	236	2 Q6PI18 HUMAN	Q6PI18 homo sapien
15	404	68.9	109	1 KV3G HUMAN	P04206 homo sapien
16	395.5	67.5	236	2 Q6P558 HUMAN	Q6P558 homo sapien
17	393	67.1	108	1 KV3A HUMAN	P01619 homo sapien
18	392	66.9	109	2 Q9UL86 HUMAN	Q9UL86 homo sapien
19	389	66.4	235	2 Q6PJF2 HUMAN	Q6PJF2 homo sapien
20	385	65.7	235	2 Q6GMV9 HUMAN	Q6GMV9 homo sapien
21	383	65.4	129	1 KV3H HUMAN	P04207 homo sapien
22	382.5	65.3	128	1 KV3K HUMAN	P06311 homo sapien
23	382	65.2	109	1 KV3F HUMAN	P01624 homo sapien
24	382	65.2	235	2 Q6GMW0 HUMAN	Q6GMW0 homo sapien
25	375.5	64.1	108	2 Q9UL70 HUMAN	Q9UL70 homo sapien
26	375	64.0	109	2 Q9UL85 HUMAN	Q9UL85 homo sapien
27	372.5	63.6	240	2 Q6PIH6 HUMAN	Q6PIH6 homo sapien
28	371.5	63.4	108	1 KV1M HUMAN	P01605 homo sapien
29	371.5	63.4	108	2 Q9UL83 HUMAN	Q9UL83 homo sapien
30	369	63.0	107	2 Q96SA9 HUMAN	Q96SA9 homo sapien
31	368.5	62.9	234	2 Q56919 HUMAN	Q56919 homo sapien

RESULT 1

ID	KV4A HUMAN	STANDARD;	PRT;	114 AA.
AC	P01625;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig kappa chain V-IV region Len.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RX	MEDLINE=76004342; PubMed=50995;			
RA	Schneider M., Hilschmann N.;			
RT	"The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).			
RN	[2]			
RP	SEQUENCE REVISION TO 9.			
RA	Salomon A.;			
RL	Submitted (AUG-1996) to Swiss-Prot.			
CC	-1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.			
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC				
DR	PDB; 1BEQ; X-ray; A/B=1-114.			
DR	PDB; 1LEU; X-ray; A/B=1-114.			
DR	PDB; 1LEQ; X-ray; A=1-114.			
DR	PDB; 1EK3; X-ray; A/B=1-114.			
DR	PDB; 1LVE; X-ray; @=1-114.			
DR	PDB; 2LVE; X-ray; @=1-114.			
DR	PDB; 3LVE; X-ray; @=1-114.			
DR	PDB; 4LVE; X-ray; A=1-114.			
DR	PDB; 5LVE; X-ray; A=1-114.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 1.			
KW	3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.			
FT	REGION 1 23 Framework-1.			
FT	REGION 24 40 Complementarity-determining-1.			
FT	REGION 41 55 Framework-2.			

ALIGNMENTS

DR	SNR; P06313; 21-133.
DR	GO; GO:0005576; C:extracellular region; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_V.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG_LIKE; 1.
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 133 Ig kappa chain V-IV region JI.
FT	REGION 21 43 Framework-1.
FT	REGION 44 60 Complementarity-determining-1.
FT	REGION 61 75 Framework-2.
FT	REGION 76 82 Complementarity-determining-2.
FT	REGION 83 114 Framework-3.
FT	REGION 115 122 Complementarity-determining-3.
FT	REGION 123 132 Framework-4.
FT	DISULFID 43 114 By similarity.
FT	NON_TER 133 133
SEQ	SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;
Query Match 78.5%; Score 460; DB 1; Length 133;	
Best Local Similarity 77.0%; Pred.No.9.8e-40;	
Matches 87; Conservative 13; Mismatches 13; Indels 0; Gaps 0;	
QY	1 EIVLTSPGSLAVSPGERVTMSKSSQSFFSSSQKNYLAWYQQIPQSPRLLIYWASTR 60 : : : : : : : :
DB	21 DIVWTQPSDLAVSLGERATINCKSSQSVLYSNNKNYLAWYQQPKQPPLIIYWASTR 80 : : : : : : : :
QY	61 ESGVDPRTFGSGSGTDTLTISVSQPEDLAIIYCHQLVLSRRTFGQTKLEIKR 113 : : : : : : : :
DB	81 ESGVDPRTFGSGSGTDTLTISLSQAEDVAIVYCCQVDITPTFGGGTKVEIKR 133 : : : : : : : :
RESULT 3	
KV4C HUMAN	
ID KV4C_HUMAN STANDARD; PRT; 134 AA.	
AC P06314;	
DT 01-JAN-1988 (Rel. 06, Created)	
DT 01-APR-1988 (Rel. 07, Last sequence update)	
DT 10-MAY-2005 (Rel. 47, Last annotation update)	
DE Ig kappa chain V-IV region B17 precursor.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;	
OC Homo.	
NCBI_TaxID=9606;	
[1]	
NUCLEOTIDE SEQUENCE.	
RX MEDLINE=86041854; PubMed=2997713;	
RA Marsh P., Mills F., Gould H.;	
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA	
RL probe.";	
RL Nucleic Acids Res. 13:6531-6544(1985).	
RL [2]	
SEQUENCE REVISION TO 76.	
RA Marsh P.;	
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.	

This Swiss-Prot entry is copyright. It is produced through a collaboration	
between the Swiss Institute of Bioinformatics and the EMBL outstation -	
the European Bioinformatics Institute. There are no restrictions on its	
use as long as its content is in no way modified and this statement is not	
removed.	

EMBL; X02990; CAA26733.1; -; mRNA.	
HSSP; P01625; ILVE.	
SMR; P06314; 21-134.	
GO; GO:0005576; C:extracellular region; NAS.	
GO; GO:0003823; F:antigen binding; NAS.	
GO; GO:0006955; P:immune response; NAS.	
InterPro; IPR007110; Ig-like.	


```

DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Framework-4.
FT REGION 122 133 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON TER 134 134 By similarity.
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 78.1%; Score 457.5; DB 1; Length 134;
Best Local Similarity 76.3%; Pred. No. 1.8e-39;
Matches 87; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVPGERVTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
DB 21 DIVMTQSPDLSAVLGRATINCKSSQSIYSSDNKNYLAWYQKQPRLLIYWASTR 80

QY 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
DB 81 ESGVPRDFSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 134

RESULT 4
Q52L64 MOUSE
ID Q52L64 MOUSE PRELIMINARY; PRT; 240 AA.
AC Q52L64;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
TX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
TX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;

```

```

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094049; AAH94049.1; -; mRNA.
DR SMR; Q52L64; 21-240.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26609 MW; CF8630CCC002E52C CRC64;

Query Match 77.2%; Score 452.5; DB 2; Length 240;
Best Local Similarity 75.4%; Pred. No. 1.2e-38;
Matches 86; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVPGERVTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
DB 21 DIVMTQSPDLSAVLGRATINCKSSQSIYSSDNKNYLAWYQKQPRLLIYWASTR 80

QY 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
DB 81 ESGVPRDFSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 134

RESULT 5
Q6KB05 MOUSE
ID Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv B8B5 protein (Fragment).
GN Name=scFv B8B5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706 (2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG LIKE; 2.
FT NON TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 74.0%; Score 433.5; DB 2; Length 255;
Best Local Similarity 76.5%; Pred. No. 1.2e-36;
Matches 88; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

QY 1 EIVLTQSPGSLAVPGERVTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
DB 137 DIVMTQSPDLSAVLGRATINCKSSQSIYSSDNKNYLAWYQKQPRLLIYWASTR 196

QY 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 112

```

```
Db 197 ESVGDPDRFTGSGSGTDTLTITSSVQAEDLAVYYCQNDHSY--PLTFGAGTKLEIK 249
RESULT 6
KV3L HUMAN
ID KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1094/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE. The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; PLO022; K3HUHA.
DR HSSP; P01625; LEEQ.
DR SMR; P18135; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JKL segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 72.5%; Score 425; DB 1; Length 129;
Best Local Similarity 73.7%; Pred. No. 4.1e-36;
Matches 84; Conservative 15; Mismatches 9; Indels 6; Gaps 3;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNTLAWYQQIPGQSPRLIYWASTR 60
Db 21 EIVLTQSPGSLSPGERATLSCRAQSV--SSS---YLAWYQKPGQAPRLIYGASSR 75

QY 61 ESVGDPDRFTGSGSGTDTLTITSSVQAEDLAIYYCHQY-ISSRTFGGQTKLEIKR 113
Db 76 ATGIPDRFSGSGSGTDTLTITSLRLEPEDFAVYYCQQYGTSPRTFGGQTKVEIKR 129

RESULT 7
KV3E HUMAN
ID KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
```

```
KV40 HUMAN
ID KV40 HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z00023; CAA77318.1; -; Genomic_DNA.
DR PIR; A01902; K4HU.
DR HSSP; P01625; LLVE.
DR SMR; P06312; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 71.7%; Score 420; DB 1; Length 121;
Best Local Similarity 78.0%; Pred. No. 1.3e-35;
Matches 78; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNTLAWYQQIPGQSPRLIYWASTR 60
Db 21 DIVMTQSPDLSAVISGERATINCKSSQSVLYSSNNKNLAWYQKPGQPKLLIYWASTR 80

QY 61 ESVGDPDRFTGSGSGTDTLTITSSVQAEDLAIYYCHQYLS 100
Db 81 ESVGDPDRFSGSGSGTDTLTITSSLSQAEDVAVYYCQQTST 120

RESULT 8
KV3E HUMAN
ID KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
```

```

group." ;
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR: A01892; K3HUS1.
DR HSSP; P01625; ILIVE.
DR SMC; P01620; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08935; IG_LIKE; 1.
DR KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
-----
Query Match 70.8%; Score 415; DB 1; Length 109;
Best Local Similarity 69.3%; Pred. No. 3.7e-35;
Matches 79; Conservative 19; Mismatches 10; Indels 6; Gaps 2;
-----
Qy 1 EIVLTQSPGSLAVPGERVMTCKSSQSVFFSSQKNYLAWYQQIPGQSPRLIYWASTR 60
Db 1 EIVLTQSPGTLSPGERATLS CRAQSQV-----SNSYLAWYQQIPGQAPRLIYCASSR 55
-----
Qy 61 ESGVPRFTGSGSGTFTLTISVQPEDIAIYYCHQYLSS-RTFGGQTKLEIKR 113
Db 56 ATGIPDRFGSGSGTFTLTISRLEPDPFAVYCYQYGGSPQTFGGQSKVEIKR 109
-----
RESULT 10
KV3M HUMAN
ID KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Klippes T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antebody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR; P18021; K3HUH1.
DR HSSP; P01625; LEEQ.

```

```
DR SMR; P18136; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Framework-2.
FT REGION 56 70 Framework-3.
FT REGION 71 77 Complementarity-determining-1.
FT REGION 78 109 Complementarity-determining-2.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JKL segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match 70.6%; Score 414; DB 1; Length 129;
Best Local Similarity 72.8%; Pred. No. 5.7e-35;
Matches 83; Conservative 15; Mismatches 10; Indels 6; Gaps 3;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKXNYLAWYQQIPGQSPRLIIYWASTR 60
Db 21 EIVLTQSPGTLSPGERATLSCRAQSV--SSS---YLAWYQKPGQAPRLIIYGASSR 75
QY 61 ESGVPRFRFGSGSGTDFTLTISVQPEDLAIIYCHQYLSSR-TFGQGTKEIKR 113
Db 76 ATGIPDRFSGSGGTDFLTISRLEPDAFYVYCOQYSGSPWTFGGGTKEIKR 129

RESULT 11
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for the
mechanism of antibody production."
RT Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC PIR; A01895; K3HUT1.
CC HSSP; P01625; ILVE.
CC SMR; P01622; 1-109.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 70.5%; Score 413; DB 1; Length 109;
Best Local Similarity 69.3%; Pred. No. 6e-35;
Matches 79; Conservative 18; Mismatches 11; Indels 6; Gaps 2;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKXNYLAWYQQIPGQSPRLIIYWASTR 60
Db 1 EIVLTQSPGTLSPGERATLSCRAQSV--SSS---YLAWYQKPGQAPRLIIYGASSR 55
QY 61 ESGVPRFRFGSGSGTDFTLTISVQPEDLAIIYCHQYLSSR-TFGQGTKEIKR 113
Db 56 ATGIPDRFSGSGGTDFLTISRLEPDAFYVYCOQYSGSPWTFGGGTKEIKR 109

RESULT 12
Q9UL78_HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1552291;
RA Martin T., Duffy S.F., Carson D.A., Kippis T.J.;
RT "Evidence for somatic selection of natural autoantibodies."
RL J. Exp. Med. 175:983-991(1992).
DR EMBL; AF035036; RAD56272.1; -; mRNA.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
```

DR	SMART; SMO0406; IGV; 1.
KW	DIRECT; PS0835; IG_LIKE; 1.
DR	Protein sequencing; Immunoglobulin domain;
KW	Immunoglobulin V region.
FQ	Framework-1.
FT	REGION 1 23
FT	REGION 24 40
FT	REGION 41 55
FT	Complementarity-determining-1.
FT	Framework-2.
FT	REGION 56 62
FT	Complementarity-determining-2.
FT	Framework-3.
FT	REGION 63 94
FT	Complementarity-determining-3.
FT	Region 95 101
FT	Complementarity-determining-4.
FT	REGION 102 109
FT	By similarity.
FT	DIULFID 23 94
FT	UNSURE 23 23
FT	UNSURE 94 94
FT	NON TER 109 109
SQ	SEQUENCE 109 AA; 12060 MW; OC4F3IEA1E1L2A0B CRC64;
Query Match 69.4%; Score 406.5; DB 1; Length 109;	
Best Local Similarity 70.6%; Pred.No.2.8e-34;	
Matches	77; Conservative 13; Mismatches 18; Indels 1; Gaps
QY	1 EIVLTQPGLAVSPGRTVMCKSSQSFFVSSOKNYLAWYQQIPGPSRLLIYWASTR 60
DB	: :
1 DIVMTQPSDLVSIGERATINCRSOSVLISNNKNYLAWYQQKPGDAPKLFSWSTR 60	:
61 ESGVPDRFTSGSGDTFLITISSVOPELAYHYCHQYLS -SRTFQGGTK 108	:
61 ESGVPDRFTSGSGDTFLITPGLQAEDVAVVYCQYYRIPTYFGCGAK 109	:
RESULT 14	
Q6PIL8 HUMAN PRELIMINARY; PRT; 236 AA.	
ID	O6PIL8 HUMAN PRELIMINARY;
AC	O6PIL8;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC	Homo.
NCBI_Taxid=9606;	[1]
TUOETIDE SEQUENCE.	
RX	MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.B., Feigold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEvann P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzyy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimwood J., Schmütz J., Myers R.M.,	
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,	
Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;	
"Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]	
TUOETIDE SEQUENCE.	
RX	MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.B., Feigold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEvann P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzyy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimwood J., Schmütz J., Myers R.M.,	
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,	
Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;	
"Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]	
TUOETIDE SEQUENCE.	
RX	MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.B., Feigold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEvann P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzyy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimwood J., Schmütz J., Myers R.M.,	
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,	
Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;	
"Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]	
TUOETIDE SEQUENCE.	
RX	MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.B., Feigold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,


```
RESULT 2
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-2

Query Match 85.2%; Score 499; DB 1; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTSCSKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
Db 1 DIQLTQSPSSSLAVSAGENVMTSCSKSSQSVLSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLSRRTFGGQTKLEIKR 113
Db 61 ESGVPRFTGSGGTDFTLTISRQVEDLAIIYCHQYLSRWTFGGGQTKLEIKR 113

RESULT 3
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-127-902-2

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTSCSKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
Db 1 DIQLTQSPSSSLAVSAGENVMTSCSKSSQSVLSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLSRRTFGGQTKLEIKR 113
Db 61 ESGVPRFTGSGGTDFTLTISRQVEDLAIIYCHQYLSRWTFGGGQTKLEIKR 113

RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
; US-09-155-107-2

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTSCSKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
```


Db 1 DIQLTSPSSLAAGENVMTMCKSSQSVLSYSAHKNYLAHYQKQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRFTGQGTGLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRFTGQGTGLEIKR 113

RESULT 5
PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 85.2%; Score 499; DB 4; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAHYQKQSPKLLIYWASTR 60
Db 1 DIQLTSPSSLAAGENVMTMCKSSQSVLSYSAHKNYLAHYQKQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRFTGQGTGLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRFTGQGTGLEIKR 113

RESULT 6
US-10-146-305-7
; Sequence 7, Application US/10146305
; Patent No. 6939956
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: OVI7440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-7

Query Match 83.4%; Score 489; DB 2; Length 130;
Best Local Similarity 82.3%; Pred. No. 8e-39;
Matches 93; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAHYQKQSPKLLIYWASTR 60
Db 1 DIVMSQSPSSLAAGENVMTMCKSSQSVLSYSAHKNYLAHYQKQSPKLLIYWASTR 60
QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRFTGQGTGLEIKR 113
Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRFTGQGTGLEIKR 113

RESULT 7
US-09-419-788-115
; Sequence 115, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-115

Query Match 83.1%; Score 487; DB 2; Length 259;
Best Local Similarity 82.3%; Pred. No. 2.6e-38;
Matches 93; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAHYQKQSPKLLIYWASTR 60
Db 141 DIVLSQSPSSLAAGENVMTMCKSSQSVLSYSAHKNYLAHYQKQSPKLLIYWASTR 200
QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRFTGQGTGLEIKR 113
Db 201 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRFTGQGTGLEIKR 253

RESULT 8
US-07-916-098A-15
; Sequence 15, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO

```

; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-435-516-4
;
Query Match 81.2%; Score 476; DB 2; Length 112;
Best Local Similarity 78.6%; Pred. No. 1.1e-37;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQPSGLAVSPGSRVMTWCKSSQSVFSSQKNYLAWYQIQPGSPRLIIYWASTR 60
Db 1 DIQLTQPSGLSASVGRDVRITTKSSQSVLYSSQKNYLAWYQKPGKAPKLLIYWASTR 60
Qy 61 ESGVPDRFTGSGSGTDTFTLISSVQPDLAIIYCHQYLSRSRTFGQGTKLEIK 112
Db 61 ESGVPSFGSGSGTDTFTFISSLQPDIAIYCHQYLSRSRTFGQGTKVEIK 112
;
RESULT 10
US-08-690-102A-6
; Sequence 6, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-690-102A-6
;
Query Match 81.2%; Score 476; DB 1; Length 113;
Best Local Similarity 78.8%; Pred. No. 1.2e-37;
Matches 89; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

```


RESULT 14

US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-14

Query Match 81.2%; Score 476; DB 1; Length 301;
Best Local Similarity 78.6%; Pred. No. 3.3e-37;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKKNLAWYQQIPGQSPRLIIYWASTR 60
DB 155 DIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNLAWYQQKPKAPKLLIYWASTR 214

QY 61 ESGVDPDRFTGSGSGTDFTLTISVQPEDLAIIYCHQYLSSRTFGQGTKEIK 112
DB 215 ESGVPSRFSGSGGTDFTTISLQPEDIAITYYCHQYLSSWTFGQGTKEIK 266

RESULT 15

US-09-188-082-14
; Sequence 14, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-14

Query Match 81.2%; Score 476; DB 2; Length 301;
Best Local Similarity 78.6%; Pred. No. 3.3e-37;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKKNLAWYQQIPGQSPRLIIYWASTR 60
DB 155 DIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNLAWYQQKPKAPKLLIYWASTR 214

QY 61 ESGVDPDRFTGSGSGTDFTLTISVQPEDLAIIYCHQYLSSRTFGQGTKEIK 112
DB 215 ESGVPSRFSGSGGTDFTTISLQPEDIAITYYCHQYLSSWTFGQGTKEIK 266

Search completed: May 9, 2006, 01:35:39
Job time : 26.4372 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 84.8723 Seconds
(without alignments)
556.303 Million cell updates/sec

Title: US-10-700-632-10
Perfect score: 586
Sequence: 1 EIVLTQSPGSLAVSPGERVT.....CHOYLSRRTFGQTKLEIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA_Main:*
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	100.0	113	5	US-10-700-632-10
2	543	92.7	113	5	US-10-700-632-8
3	543	92.7	114	5	US-10-700-632-62
4	511	87.2	112	4	US-10-229-335-28
5	510	87.0	113	5	US-10-722-849-4
6	510	87.0	113	6	US-11-004-659-4
7	510	87.0	133	5	US-10-723-003-10
8	510	87.0	133	6	US-11-004-639-10
9	510	87.0	239	5	US-10-723-003-14
10	510	87.0	239	6	US-11-004-639-14
11	510	87.0	661	5	US-10-723-003-34
12	510	87.0	661	6	US-11-004-639-34
13	509	86.9	112	4	US-10-056-052-10
14	509	86.9	112	5	US-10-816-938-31
15	508	86.7	112	4	US-10-056-052-6
16	507	86.5	112	4	US-10-056-052-18
17	503	85.8	112	4	US-10-056-052-14
18	499	85.2	113	3	US-09-741-843-2
19	499	85.2	113	3	US-09-894-839-2
20	499	85.2	113	3	US-09-988-013A-2
21	499	85.2	113	4	US-10-446-689-2
22	499	85.2	113	5	US-10-787-378-2
23	499	85.2	113	5	US-10-974-678-2
24	499	85.2	272	4	US-10-207-655-14
25	499	85.2	272	4	US-10-053-530-14
26	499	85.2	272	6	US-11-089-511-14
27	499	85.2	272	6	US-11-089-190-14

28	499	85.2	272	6	US-11-088-570-14	Sequence 14, Appl
29	499	85.2	272	6	US-11-088-737-14	Sequence 14, Appl
30	499	85.2	272	6	US-11-088-569-14	Sequence 14, Appl
31	499	85.2	272	6	US-11-088-693-14	Sequence 14, Appl
32	499	85.2	272	6	US-11-089-367-14	Sequence 14, Appl
33	499	85.2	272	6	US-11-089-368-14	Sequence 14, Appl
34	497	84.8	132	6	US-11-013-537-2	Sequence 2, Appl
35	497	84.8	132	6	US-11-013-537-1	Sequence 1, Appl
36	489	83.4	130	4	US-10-146-305-7	Sequence 7, Appl
37	478	81.6	238	4	US-10-467-253-14	Sequence 14, Appl
38	477.5	81.5	146	5	US-10-830-899-56	Sequence 56, Appl
39	477.5	81.5	146	5	US-10-830-899-63	Sequence 63, Appl
40	477.5	81.5	146	5	US-10-861-662-56	Sequence 56, Appl
41	477.5	81.5	146	5	US-10-861-662-63	Sequence 63, Appl
42	476	81.2	112	4	US-10-229-335-4	Sequence 4, Appl
43	476	81.2	352	3	US-09-203-958A-2	Sequence 2, Appl
44	476	81.2	352	5	US-10-764-131-2	Sequence 2, Appl
45	473	80.7	112	4	US-10-467-253-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-700-632-10
; Sequence 10, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region
US-10-700-632-10

Query Match 100.0%; Score 586; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSQSVFFSSQKNYLAWYQOI PQSPRLLIYWASTR 60
Db 1 EIVLTQSPGSLAVSPGERVTMSCKSQSVFFSSQKNYLAWYQOI PQSPRLLIYWASTR 60
QY 61 ESGVDPDRFTGSGSGDFTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113
Db 61 ESGVDPDRFTGSGSGDFTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

RESULT 2
US-10-700-632-8
; Sequence 8, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-8

Query Match      92.7%; Score 543; DB 5; Length 113;
Best Local Similarity 93.8%; Pred. No. 2.6e-39;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY  2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  2 IMVTQSPSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  62 SGVPDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 3
US-10-700-632-62
; Sequence 62, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62

Query Match      92.7%; Score 543; DB 5; Length 114;
Best Local Similarity 93.8%; Pred. No. 2.6e-39;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY  2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  2 IMLTQSPSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  62 SGVPDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 4
US-10-229-335-28
; Sequence 28, Application US/10229335
; Publication No. US2003014483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,335
; FILING DATE: 26-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match      87.2%; Score 511; DB 4; Length 112;
Best Local Similarity 88.3%; Pred. No. 1.5e-36;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY  2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  2 IVMTQSPSSLAVSAGEKVTMCKSSQSVLYSSQKNYLAWYQIQGSPKLLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 112
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  62 SGVPDRFTGSGSGTDTLTITSSVQAEADLAIIYCHQYLSRRTFGGKLEIKR 112
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 5
US-10-722-849-4
; Sequence 4, Application US/10722849
; Publication No. US20050031617A1
; GENERAL INFORMATION:
; APPLICANT: WA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/10/722,849
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-722-849-4

Query Match      87.0%; Score 510; DB 5; Length 113;
Best Local Similarity 86.6%; Pred. No. 1.8e-36;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY  2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  2 IMVTQSPSSLAVSAGEKVTMCKSSQSVLYSSQKNYLAWYQIQGSPKLLIYWASTRE 61
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY  62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  62 SGVPDRFTGSGSGTDTLTITSSVQAEADLAIIYCHQYLSRRTFGGKLEIKR 113
    |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 6
```

```

RESULT 8
US-11-004-639-10
; Sequence 10, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-10

Query Match      87.0%; Score 510; DB 6; Length 133;
Best Local Similarity 86.6%; Pred. No. 2.le-36;
Matches 97; Conservative 7; Mismatches 8; Indels

Qy    2   IVLTSQPSGLAVSGRVTMSCKSSQSVPFSSQKNYLAWYQIIPGQSPSR
       |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    22  IMMTQSPSSLVSAAGEKVITMSCKSSQSVLYSSNQKNYLAWYQQKPGQSP

```

```

Db      82  SGVPDRPTSGSGTDFLTLTSSVQAEADLAVVYCHQVPSSTFGGKTLEIKR 133

RESULT 9
US-10-723-003-14
; Sequence 14, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14

Query Match      87.0%; Score 510; DB 5; Length 239;
Best Local Similarity 86.6%; Pred. No. 3 8e-36;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      2  IVLTQSPGSLAVSPGSRVTMSCKSSQSVTFSSQKNYLAWYQOI PQGSPRLIIYWASTRE 61
Db      22  IMVTQSPGSLAVSAGEKVTMSCKSSQSVLYSSNKNYLAWYQOKPGSPKLLIYWASTRE 81

```

```
QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHOYLSRRTFGQGTKEIKR 113
Db 82 SGVPRFTGSGSGTDTLTITSSVQABDLAVYYCHQYFSSYTFGGGTKEIKR 133

RESULT 10
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14

Query Match 87.0%; Score 510; DB 6; Length 239;
Best Local Similarity 86.6%; Pred. No. 3.8e-36;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAIIYCHOYLSRRTFGQGTKEIKR 61
Db 22 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAIIYCHOYLSRRTFGQGTKEIKR 81

QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHOYLSRRTFGQGTKEIKR 113
Db 82 SGVPRFTGSGSGTDTLTITSSVQABDLAVYYCHQYFSSYTFGGGTKEIKR 133

RESULT 11
US-10-723-003-34
; Sequence 34, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-34

Query Match 87.0%; Score 510; DB 5; Length 661;
```

```
Best Local Similarity 86.6%; Pred. No. 1e-35;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAIIYCHOYLSRRTFGQGTKEIKR 61
Db 550 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAIIYCHOYLSRRTFGQGTKEIKR 609

QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHOYLSRRTFGQGTKEIKR 113
Db 610 SGVPRFTGSGSGTDTLTITSSVQABDLAVYYCHQYFSSYTFGGGTKEIKR 661

RESULT 12
US-11-004-639-34
; Sequence 34, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-34

Query Match 87.0%; Score 510; DB 6; Length 661;
Best Local Similarity 86.6%; Pred. No. 1e-35;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAIIYCHOYLSRRTFGQGTKEIKR 61
Db 550 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAIIYCHOYLSRRTFGQGTKEIKR 609

QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHOYLSRRTFGQGTKEIKR 113
Db 610 SGVPRFTGSGSGTDTLTITSSVQABDLAVYYCHQYFSSYTFGGGTKEIKR 661

RESULT 13
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
```


THIS PAGE BLANK (uspto)


```

; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
; US-11-096-046-29

Query Match      88.1%; Score 516; DB 11; Length 667;
Best Local Similarity 86.7%; Pred. No. 3.1e-30;
Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGSLAVSPGERVTMTCKSSQSVFPFSSQKNYLAWYQOIPGQSPRLIIYWASTR 60
Db 1 DMMTQSPSLAVSAGEKVTMTCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60

Qy 61 ESGVPRDFTGSGGTDFTLTITISSVQPEDLAIVYCHQVLSRTFGQGTGLEIKR 113
Db 61 ESGVPRDFTGSGGTDFTLTITISSVQAEADLAIVYCHQVLSRTFGGKTGLEIKR 113

RESULT 5
US-11-136-559-10
; Sequence 10, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-11-136-559-10

Query Match      86.9%; Score 509; DB 11; Length 112;
Best Local Similarity 87.4%; Pred. No. 2.5e-30;
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IVLTSQPSGLAVSPGERVTMTCKSSQSVFPFSSQKNYLAWYQOIPGQSPRLIIYWASTRE 61
Db 2 IMMTQSPSLAVSAGEKVTMTCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTRE 61

```



```
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; TYPE: PRT
; LENGTH: 112
; ORGANISM: Staphylococcus aureus
; OTHER INFORMATION:
US-11-136-559-22

Query Match      84.6%; Score 496; DB 11; Length 112;
Best Local Similarity 85.6%; Pred. No. 2.2e-29;
Matches 95; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTPSGSLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLLIYWASTRE 61
Db 2 IMWTQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTRE 61

QY 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 112
Db 62 SGVPDRFTGSGGTDFTLTISVQAEADLAVYCHQYLSYTFGGTKEIKR 112

RESULT 10
US-10-512-184-31
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match      82.2%; Score 481.5; DB 9; Length 259;
Best Local Similarity 82.5%; Pred. No. 4.5e-28;
Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 138 DIVLSQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTR 197

QY 61 ESGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
```

```
Db 198 ESGVPDRFTGSGGTDFTLTISVKAEDLAVYCOQYYSYPTFGSGTKLEIKR 251

RESULT 11
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match      82.2%; Score 481.5; DB 9; Length 329;
Best Local Similarity 82.5%; Pred. No. 5.4e-28;
Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 208 DIVLSQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTR 267

QY 61 ESGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 268 ESGVPDRFTGSGGTDFTLTISVKAEDLAVYCOQYYSYPTFGSGTKLEIKR 321

RESULT 12
US-10-981-356A-3
; Sequence 3, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-3

Query Match      81.2%; Score 476; DB 9; Length 116;
Best Local Similarity 77.0%; Pred. No. 6e-28;
Matches 87; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 1 DIQMTQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGKAPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 61 ESGVPSRFSGSGGTDFTLTISSLQPEDFATYYCHQYLSSDTFGGQGTKEIKR 113
```


THIS PAGE BLANK (USPTO)